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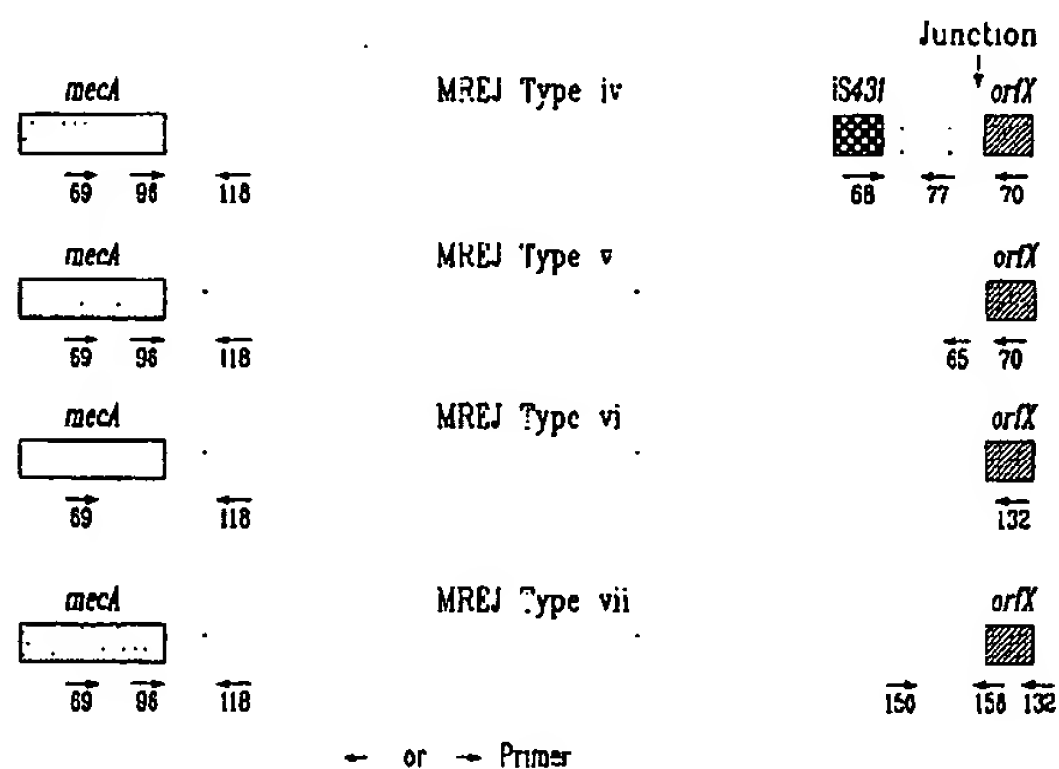
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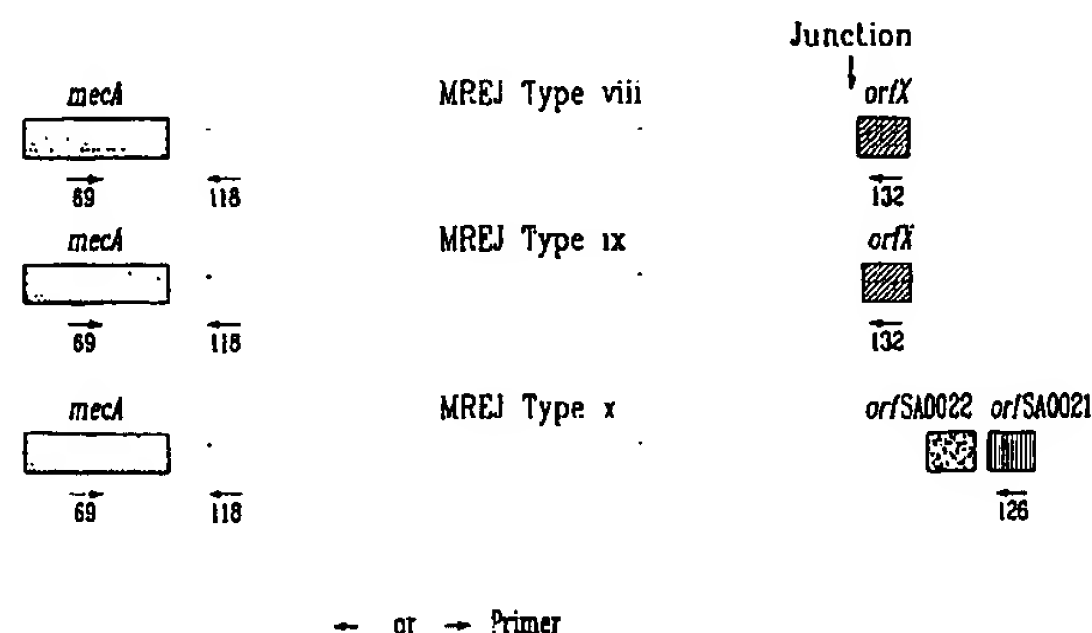
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(54) Title: SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS*



(57) Abstract: The present invention describes novel SCCmec right extremity junction sequences for the detection of methicillin-resistant *Staphylococcus aureus* (MRSA). It relates to the use of these DNA sequences for diagnostic purposes.



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SEQUENCES FOR DETECTION AND IDENTIFICATION OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS*

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BACKGROUND OF THE INVENTION

Clinical significance of *Staphylococcus aureus*

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The coagulase-positive species *Staphylococcus aureus* is well documented as a human opportunistic pathogen. Nosocomial infections caused by *S. aureus* are a major cause of morbidity and mortality. Some of the most common infections caused by *S. aureus* involve the skin, and they include furuncles or boils, cellulitis, impetigo, and postoperative wound infections at various sites. Some of the more serious infections produced by *S. aureus* are bacteremia, pneumonia, osteomyelitis, acute endocarditis, myocarditis, pericarditis, cerebritis, meningitis, scalded skin syndrome, and various abscesses. Food poisoning mediated by staphylococcal enterotoxins is another important syndrome associated with *S. aureus*. Toxic shock syndrome, a community-acquired disease, has also been attributed to infection or colonization with toxigenic *S. aureus* (Murray *et al.* Eds, 1999, Manual of Clinical Microbiology, 7th Ed., ASM Press, Washington, D.C.).

Methicillin-resistant *S. aureus* (MRSA) emerged in the 1980s as a major clinical and epidemiologic problem in hospitals. MRSA are resistant to all β -lactams including penicillins, cephalosporins, carbapenems, and monobactams, which are the most commonly used antibiotics to cure *S. aureus* infections. MRSA infections can only be treated with more toxic and more costly antibiotics, which are normally used as the last line of defence. Since MRSA can spread easily from patient to patient via personnel, hospitals over the world are confronted with the

problem to control MRSA. Consequently, there is a need to develop rapid and simple screening or diagnostic tests for detection and/or identification of MRSA to reduce its dissemination and improve the diagnosis and treatment of infected patients.

5

Methicillin resistance in *S. aureus* is unique in that it is due to acquisition of DNA from other coagulase-negative staphylococci (CNS), coding for a supernumerary β -lactam-resistant penicillin-binding protein (PBP), which takes over the biosynthetic functions of the normal PBPs when the cell is exposed to β -lactam antibiotics. *S. aureus* normally contains four PBPs, of which PBPs 1, 2 and 3 are essential. The low-affinity PBP in MRSA, termed PBP 2a (or PBP2'), is encoded by the chromosomal *mecA* gene and functions as a β -lactam-resistant transpeptidase. The *mecA* gene is absent from methicillin-sensitive *S. aureus* but is widely distributed among other species of staphylococci and is highly conserved (Ubukata *et al.*, 1990, Antimicrob. Agents Chemother. **34**:170-172).

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15

By nucleotide sequence determination of the DNA region surrounding the *mecA* gene from *S. aureus* strain N315 (isolated in Japan in 1982), Hiramatsu *et al.* have found that the *mecA* gene is carried by a novel genetic element, designated staphylococcal cassette chromosome *mec* (SCC*mec*), inserted into the chromosome. SCC*mec* is a mobile genetic element characterized by the presence of terminal inverted and direct repeats, a set of site-specific recombinase genes (*ccrA* and *ccrB*), and the *mecA* gene complex (Ito *et al.*, 1999, Antimicrob. Agents Chemother. **43**:1449-1458; Katayama *et al.*, 2000, Antimicrob. Agents Chemother. **44**:1549-1555). The element is precisely excised from the chromosome of *S. aureus* strain N315 and integrates into a specific *S. aureus* chromosomal site in the same orientation through the function of a unique set of recombinase genes comprising *ccrA* and *ccrB*. Two novel genetic elements that shared similar structural features of SCC*mec* were found by cloning and sequencing the DNA

20
25

region surrounding the *mecA* gene from MRSA strains NCTC 10442 (the first MRSA strain isolated in England in 1961) and 85/2082 (a strain from New Zealand isolated in 1985). The three SCC*mec* have been designated type I (NCTC 10442), type II (N315) and type III (85/2082) based on the year of isolation of the strains (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336) (Figure 1). Hiramatsu *et al.* have found that the SCC*mec* DNAs are integrated at a specific site in the methicillin-sensitive *S. aureus* (MSSA) chromosome. They characterized the nucleotide sequences of the regions around the left and right boundaries of SCC*mec* DNA (i.e. *attL* and *attR*, respectively) as well as those of the regions around the SCC*mec* DNA integration site (i.e. *attB_{scc}* which is the bacterial chromosome attachment site for SCC*mec* DNA). The *attB_{scc}* site was located at the 3' end of a novel open reading frame (ORF), *orfX*. The *orfX* potentially encodes a 159-amino acid polypeptide sharing identity with some previously identified polypeptides, but of unknown function (Ito *et al.*, 1999, Antimicrob. Agents Chemother. **43**:1449-1458). Recently, a new type of SCC*mec* (type IV) has been described by both Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) and Oliveira *et al.* (Oliveira *et al.*, 2001, Microb. Drug Resist. **7**:349-360). The sequences of the right extremity of the new type IV SCC*mec* from *S. aureus* strains CA05 and 8/6-3P published by Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152) were nearly identical over 2000 nucleotides to that of type II SCC*mec* of *S. aureus* strain N315 (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336). No sequence at the right extremity of the SCC*mec* type IV is available from the *S. aureus* strains HDE288 and PL72 described by Oliveira *et al.* (Oliveira *et al.*, 2001, Microb. Drug Resist. **7**:349-360).

Previous methods used to detect and identify MRSA (Saito *et al.*, 1995, J. Clin. Microbiol. **33**:2498-2500; Ubukata *et al.*, 1992, J. Clin. Microbiol. **30**:1728-1733; Murakami *et al.*, 1991, J. Clin. Microbiol. **29**:2240-2244; Hiramatsu *et al.*, 1992,

Microbiol. Immunol. 36:445-453), which are based on the detection of the *mecA* gene and *S. aureus*-specific chromosomal sequences, encountered difficulty in discriminating MRSA from methicillin-resistant coagulase-negative staphylococci (CNS) because the *mecA* gene is widely distributed in both *S. aureus* and CNS species (Suzuki *et al.*, 1992, Antimicrob. Agents. Chemother. 36:429-434). Hiramatsu *et al.* (US patent 6,156,507) have described a PCR assay specific for MRSA by using primers that can specifically hybridize to the right extremities of the 3 types of SCC*mec* DNAs in combination with a primer specific to the *S. aureus* chromosome, which corresponds to the nucleotide sequence on the right side of the SCC*mec* integration site. Since nucleotide sequences surrounding the SCC*mec* integration site in other staphylococcal species (such as *S. epidermidis* and *S. haemolyticus*) are different from those found in *S. aureus*, this PCR assay was specific for the detection of MRSA. This PCR assay also supplied information for MREP typing (standing for «*mec* right extremity polymorphism») of SCC*mec* DNA (Ito *et al.*, 2001, Antimicrob. Agents Chemother. 45:1323-1336; Hiramatsu *et al.*, 1996, J. Infect. Chemother. 2:117-129). This typing method takes advantage of the polymorphism at the right extremity of SCC*mec* DNAs adjacent to the integration site among the three types of SCC*mec*. Type III has a unique nucleotide sequence while type II has an insertion of 102 nucleotides to the right terminus of SCC*mec* type I. The MREP typing method described by Hiramatsu *et al.* (Ito *et al.*, 2001, Antimicrob. Agents Chemother. 45:1323-1336; Hiramatsu *et al.*, 1996, J. Infect. Chemother. 2:117-129) defines the SCC*mec* type I as MREP type i, SCC*mec* type II as MREP type ii and SCC*mec* type III as MREP type iii. It should be noted that the MREP typing method cannot differentiate the new SCC*mec* type IV described by Hiramatsu *et al.* (Ma *et al.*, 2002, Antimicrob. Agents Chemother. 46:1147-1152) from SCC*mec* type II because these two SCC*mec* types exhibit the same nucleotide sequence to the right extremity.

The set of primers described by Hiramatsu et al. as being the optimal primer combination (SEQ ID NOs.: 22, 24, 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) have been used in the present invention to test by PCR a variety of MRSA and MSSA strains
5 (Figure 1 and Table 1). Twenty of the 39 MRSA strains tested were not amplified by the Hiramatsu et al. multiplex PCR assay (Tables 2 and 3). Hiramitsu's method indeed was successful in detecting less than 50% of the tested 39 MRSA strains. This finding demonstrates that some MRSA strains have sequences at the right extremity of SCC*mec*-chromosome right extremity junction different from those
10 identified by Hiramatsu *et al.* Consequently, the system developed by Hiramatsu *et al.* does not allow the detection of all MRSA. The present invention relates to the generation of SCC*mec*-chromosome right extremity junction sequence data required to detect more MRSA strains in order to improve the Hiramatsu *et al.* assay. There is a need for developing more ubiquitous primers and probes for the
15 detection of most MRSA strains around the world.

SUMMARY OF THE INVENTION

20 It is an object of the present invention to provide a specific, ubiquitous and sensitive method using probes and/or amplification primers for determining the presence and/or amount of nucleic acids from all MRSA strains.

Ubiquity of at least 50% amongst the strains representing MRSA strains types IV
25 to X is an objective of this invention.

Therefore, in accordance with the present invention is provided a method to detect the presence of a methicillin-resistant *Staphylococcus aureus* (MRSA) strain in a sample, the MRSA strain being resistant because of the presence of an SCC*mec*

insert containing a *mecA* gene, said *SCC_{mec}* being inserted in bacterial nucleic acids thereby generating a polymorphic right extremity junction (MREJ), the method comprising the step of annealing the nucleic acids of the sample with a plurality of probes and/or primers, characterized by:

- 5 (i) the primers and/or probes are specific for MRSA strains and capable of annealing with polymorphic MREJ nucleic acids, the polymorphic MREJ comprising MREJ types i to x; and
 - (ii) the primers and/or probes altogether can anneal with at least four MREJ types selected from MREJ types i to x.
- 10 In a specific embodiment, the primers and/or probes are all chosen to anneal under common annealing conditions, and even more specifically, they are placed altogether in the same physical enclosure.

A specific method has been developed using primers and/or probes having at least 10 nucleotides in length and capable of annealing with MREJ types i to iii, defined
 15 in any one of SEQ ID NOs: 1, 20, 21, 22, 23, 24, 25, 41, 199 ; 2, 17, 18, 19, 26, 40, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 185, 186, 197 ; 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 104, 184, 198 and with one or more of MREJ types iv to ix, having SEQ ID NOs: 42, 43, 44, 45, 46, 51 ; 47, 48, 49, 50 ; 171 ; 165, 166 ; 167 ; 168. To be perfectly ubiquitous with the all the sequenced MREJs, the
 20 primers and/or probes altogether can anneal with said SEQ ID NOs of MREJ types i to ix.

The following specific primers and/or probes having the following sequences have been designed:

| | | |
|----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|
| 25 30 | 66, 100, 101, 105, 52, 53, 54, 55, 56, 57, 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159, 59, 62, 126, 127, 128, 129, 131, 200, 201, 60, 61, 63 32, 83, 84, 160, 161, 162, 163, 164 85, 86, 87, 88, 89 | for the detection of MREJ type i |
|----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|

66, 97, 99, 100, 101, 106, 117, for the detection of MREJ type ii
 118, 124, 125, 52, 53, 54, 55, 56, 57
 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 5 59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 10 85, 86, 87, 88, 89

67, 98, 102, 107, 108 for the detection of MREJ type iii
 64, 71, 72, 73, 74, 75, 76, 70,
 103, 130, 132, 158, 159
 15 58,
 59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 20 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

79, 77, 145, 147 for the detection of MREJ type iv
 64, 71, 72, 73, 74, 75, 76, 70,
 25 103, 130, 132, 158, 159
 59, 62
 126, 127
 128, 129, 131, 200, 201
 60, 61, 63
 30 68
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

65, 80, 146, 154, 155 for the detection of MREJ type v
 35 64, 71, 72, 73, 74, 75, 76,
 70, 103, 130, 132, 158, 159
 59, 62
 126, 127
 128, 129, 131, 200, 201
 40 60, 61, 63
 32, 83, 84, 160, 161, 162, 163, 164
 85, 86, 87, 88, 89

202, 203, 204
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
5 126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89

for the detection of MREJ type vi

10

112, 113, 114, 119, 120, 121, 122
123, 150, 151, 153
64, 71, 72, 73, 74, 75, 76, 70, 103,
130, 132, 158, 159
15 59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
20 85, 86, 87, 88, 89

for the detection of MREJ type vii,

115, 116, 187, 188, 207, 208
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
25 59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
30 85, 86, 87, 88, 89

for the detection of MREJ type viii

109, 148, 149, 205, 206
64, 71, 72, 73, 74, 75, 76
70, 103, 130, 132, 158, 159
35 59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
40 85, 86, 87, 88, 89

for the detection of MREJ type ix.

Amongst these, the following primer pairs having the following sequences are used:

- | | | |
|----|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------|
| 5 | 64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57 | for the detection of type i MREJ |
| 10 | 64/66, 64/97, 64/99, 64/100, 64/101 | for the detection of type ii MREJ |
| 15 | 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 63/53, 63/54, 63/55, 63/56, 63/57 | |
| 20 | 64/67, 64/98, 64/102 ; 59/58, 60/58, 61/58, 62/58, 63/58 | for the detection of type iii MREJ |
| | 64/79 | for the detection of type iv MREJ |
| | 64/80 | for the detection of type v MREJ |
| | 64/204 | for the detection of type vi MREJ |
| 25 | 64/112, 64/113 | for the detection of type vii MREJ |
| | 64/115, 64/116 | for the detection of type viii MREJ |
| | 64/109 | for the detection of type ix MREJ |

As well, amongst these, the following probes having the following sequences are used:

SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164 for the detection of MREJ types i to ix.

In the most preferred embodied method, the following primers and/or probes having the following nucleotide sequences are used together. The preferred combinations make use of:

- 5 i) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type i
- ii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type ii
- iii) SEQ ID NOs: 64, 67, 84, 163, 164 for the detection of MREJ type iii
- iv) SEQ ID NOs: 64, 79, 84, 163, 164 for the detection of MREJ type iv
- v) SEQ ID NOs: 64, 80, 84, 163, 164 for the detection of MREJ type v
- 10 vi) SEQ ID NOs: 64, 112, 84, 163, 164 for the detection of MREJ type
 vii.

All these probes and primers can even be used together in the same physical enclosure.

- 15 It is another object of this invention to provide a method for typing a MREJ of a MRSA strain, which comprises the steps of: reproducing the above method with primers and/or probes specific for a determined MREJ type, and detecting an annealed probe or primer as an indication of the presence of a determined MREJ type.

- 20 It is further another object of this invention to provide a nucleic acid selected from SEQ ID NOs:

- i) SEQ ID NOs: 42, 43, 44, 45, 46, 51 for sequence of MREJ type iv ;
- ii) SEQ ID NOs: 47, 48, 49, 50 for sequence of MREJ type v ;
- iii) SEQ ID NOs: 171 for sequence of MREJ type vi ;
- 25 iv) SEQ ID NOs: 165, 166 for sequence of MREJ type vii ;
- v) SEQ ID NOs: 167 for sequence of MREJ type viii ;
- vi) SEQ ID NOs: 168 for sequence of MREJ type ix.

Oligonucleotides of at least 10 nucleotides in length which hybridize with any of these nucleic acids and which hybridize with one or more MREJ of types selected from iv to ix are also objects of this invention. Amongst these, primer pairs (or probes) having the following SEQ ID NOs:

- 5 64/66, 64/100, 64/101; 59/52, for the detection of type i MREJ
 59/53, 59/54, 59/55, 59/56, 59/57,
 60/52, 60/53, 60/54, 60/55, 60/56
 60/57, 61/52, 61/53, 61/54, 61/55
 61/56, 61/57, 62/52, 62/53, 62/54
 10 62/55, 62/56, 62/57, 63/52, 63/53
 63/54, 63/55, 63/56, 63/57
- 64/66, 64/97, 64/99, 64/100, 64/101 for the detection of type ii MREJ
 59/52, 59/53, 59/54, 59/55, 59/56,
 15 59/57, 60/52, 60/53, 60/54, 60/55,
 60/56, 60/57, 61/52, 61/53, 61/54,
 61/55, 61/56, 61/57, 62/52, 62/53,
 62/54, 62/55, 62/56, 62/57, 63/52
 63/53, 63/54, 63/55, 63/56, 63/57
 20
- 64/67, 64/98, 64/102 ; 59/58, for the detection of type iii MREJ
 60/58, 61/58, 62/58, 63/58
- 64/79 for the detection of type iv MREJ
 25 64/80 for the detection of type v MREJ
 64/204 for the detection of type vi MREJ
 64/112, 64/113 for the detection of type vii MREJ
 64/115, 64/116 for the detection of type viii MREJ
 64/109 for the detection of type ix MREJ,
 30 are also within the scope of this invention.

Further, internal probes having nucleotide sequences defined in any one of SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164, are also within the scope of this invention.

Compositions of matter comprising the primers and/or probes annealing or hybridizing with one or more MREJ of types selected from iv to ix as well as with
 5 the above nucleic acids, comprising or not primers and/or probes, which hybridize with one or more MREJ of types selected from i to iii, are further objects of this invention. The preferred compositions would comprise the primers having the nucleotide sequences defined in SEQ ID NOs:

64/66, 64/100, 64/101; 59/52, for the detection of type i MREJ
 10 59/53, 59/54, 59/55, 59/56, 59/57,
 60/52, 60/53, 60/54, 60/55, 60/56
 60/57, 61/52, 61/53, 61/54, 61/55
 61/56, 61/57, 62/52, 62/53, 62/54
 62/55, 62/56, 62/57, 63/52, 63/53
 15 63/54, 63/55, 63/56, 63/57

64/66, 64/97, 64/99, 64/100, 64/101 for the detection of type ii MREJ
 59/52, 59/53, 59/54, 59/55, 59/56,
 59/57, 60/52, 60/53, 60/54, 60/55,
 20 60/56, 60/57, 61/52, 61/53, 61/54,
 61/55, 61/56, 61/57, 62/52, 62/53,
 62/54, 62/55, 62/56, 62/57, 63/52
 63/53, 63/54, 63/55, 63/56, 63/57

25 64/67, 64/98, 64/102 ; 59/58, for the detection of type iii MREJ
 60/58, 61/58, 62/58, 63/58

64/79 for the detection of type iv MREJ
 64/80 for the detection of type v MREJ
 30 64/204 for the detection of type vi MREJ
 64/112, 64/113 for the detection of type vii MREJ
 64/115, 64/116 for the detection of type viii MREJ
 64/109 for the detection of type ix MREJ,

or probes, which SEQ ID NOs are: 32, 83, 84, 160, 161, 162, 163, 164, or both.

5

DETAILED DESCRIPTION OF THE INVENTION

Here is particularly provided a method wherein each of MRSA nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said primers or probes developed to be ubiquitous;

10 wherein each of said nucleic acids or a variant or part thereof comprises a selected target region hybridizable with said primers or probes ;

 said method comprising the steps of contacting said sample with said probes or primers and detecting the presence and/or amount of hybridized probes or amplified products as an indication of the presence and/or amount of MRSA.

15

In the method, sequences from DNA fragments of SCC*mec*-chromosome right extremity junction, thereafter named MREJ standing for « *mec* right extremity junction » including sequences from SCC*mec* right extremity and chromosomal DNA to the right of the SCC*mec* integration site are used as parental sequences
20 from which are derived the primers and/or the probes. MREJ sequences include our proprietary sequences as well as sequences obtained from public databases and from US patent 6,156,507 and were selected for their capacity to sensitively, specifically, ubiquitously and rapidly detect the targeted MRSA nucleic acids.

25 Our proprietary DNA fragments and oligonucleotides (primers and probes) are also another object of this invention.

Composition of matters such as diagnostic kits comprising amplification primers or probes for the detection of MRSA are also objects of the present invention.

In the above methods and kits, probes and primers are not limited to nucleic acids and may include, but are not restricted to, analogs of nucleotides. The diagnostic reagents constituted by the probes and the primers may be present in any suitable
5 form (bound to a solid support, liquid, lyophilized, etc.).

In the above methods and kits, amplification reactions may include but are not restricted to: a) polymerase chain reaction (PCR), b) ligase chain reaction (LCR), c) nucleic acid sequence-based amplification (NASBA), d) self-sustained sequence
10 replication (3SR), e) strand displacement amplification (SDA), f) branched DNA signal amplification (bDNA), g) transcription-mediated amplification (TMA), h) cycling probe technology (CPT), i) nested PCR, j) multiplex PCR, k) solid phase amplification (SPA), l) nuclease dependent signal amplification (NDSA), m) rolling circle amplification technology (RCA), n) Anchored strand displacement
15 amplification, o) Solid-phase (immobilized) rolling circle amplification.

In the above methods and kits, detection of the nucleic acids of target genes may include real-time or post-amplification technologies. These detection technologies can include, but are not limited to fluorescence resonance energy transfer (FRET)-
20 based methods such as adjacent hybridization of probes (including probe-probe and probe-primer methods), *TaqMan* probe, molecular beacon probe, Scorpion probe, nanoparticle probe and Amplifluor probe. Other detection methods include target gene nucleic acids detection via immunological methods, solid phase hybridization methods on filters, chips or any other solid support. In these systems,
25 the hybridization can be monitored by fluorescence, chemiluminescence, potentiometry, mass spectrometry, plasmon resonance, polarimetry, colorimetry, flow cytometry or scanometry. Nucleotide sequencing, including sequencing by dideoxy termination or sequencing by hybridization (e.g. sequencing using a DNA

chip) represents another method to detect and characterize the nucleic acids of target genes.

In a preferred embodiment, a PCR protocol is used for nucleic acid amplification.

5

A method for detection of a plurality of potential MRSA strains having different MREJ types may be conducted in separate reactions and physical enclosures, one type at the time. Alternatively, it could be conducted simultaneously for different types in separate physical enclosures, or in the same physical enclosures. In the
10 latter scenario a multiplex PCR reaction could be conducted which would require that the oligonucleotides are all capable of annealing with a target region under common conditions. Since many probes or primers are specific for a determined MREJ type, typing a MRSA strain is a possible embodiment. When a mixture of oligonucleotides annealing together with more than one type is used in a single
15 physical enclosure or container, different labels would be used to distinguish one type from another.

We aim at developing a DNA-based test or kit to detect and identify MRSA. Although the sequences from *orfX* genes and some *SCCmec* DNA fragments are
20 available from public databases and have been used to develop DNA-based tests for detection of MRSA, new sequence data allowing to improve MRSA detection and identification which are object of the present invention have either never been characterized previously or were known but not shown to be located at the right extremity of *SCCmec* adjacent to the integration site (Table 4). These novel
25 sequences could not have been predicted nor detected by the MRSA-specific PCR assay developed by Hiramatsu *et al.* (US patent 6,156,507). These sequences will allow to improve current DNA-based tests for the diagnosis of MRSA because they allow the design of ubiquitous primers and probes for the detection and

identification of more MRSA strains including all the major epidemic clones from around the world.

The diagnostic kits, primers and probes mentioned above can be used to detect
5 and/or identify MRSA, whether said diagnostic kits, primers and probes are used for *in vitro* or *in situ* applications. The said samples may include but are not limited to: any clinical sample, any environmental sample, any microbial culture, any microbial colony, any tissue, and any cell line.

10 It is also an object of the present invention that said diagnostic kits, primers and probes can be used alone or in combination with any other assay suitable to detect and/or identify microorganisms, including but not limited to: any assay based on nucleic acids detection, any immunoassay, any enzymatic assay, any biochemical
15 assay, any lysotypic assay, any serological assay, any differential culture medium, any enrichment culture medium, any selective culture medium, any specific assay medium, any identification culture medium, any enumeration culture medium, any cellular stain, any culture on specific cell lines, and any infectivity assay on animals.

20 In the methods and kits described herein below, the oligonucleotide probes and amplification primers have been derived from larger sequences (i.e. DNA fragments of at least 100 base pairs). All DNA sequences have been obtained either from our proprietary sequences or from public databases (Tables 5, 6, 7, 8 and 9).

25

It is clear to the individual skilled in the art that oligonucleotide sequences other than those described in the present invention and which are appropriate for detection and/or identification of MRSA may also be derived from the proprietary fragment sequences or selected public database sequences. For example, the

oligonucleotide primers or probes may be shorter but of a length of at least 10 nucleotides or longer than the ones chosen; they may also be selected anywhere else in the proprietary DNA fragments or in the sequences selected from public databases; they may also be variants of the same oligonucleotide. If the target
5 DNA or a variant thereof hybridizes to a given oligonucleotide, or if the target DNA or a variant thereof can be amplified by a given oligonucleotide PCR primer pair, the converse is also true; a given target DNA may hybridize to a variant oligonucleotide probe or be amplified by a variant oligonucleotide PCR primer. Alternatively, the oligonucleotides may be designed from said DNA fragment
10 sequences for use in amplification methods other than PCR. Consequently, the core of this invention is the detection and/or identification of MRSA by targeting genomic DNA sequences which are used as a source of specific and ubiquitous oligonucleotide probes and/or amplification primers. Although the selection and evaluation of oligonucleotides suitable for diagnostic purposes require much effort,
15 it is quite possible for the individual skilled in the art to derive, from the selected DNA fragments, oligonucleotides other than the ones listed in Tables 5, 6, 7, 8 and 9 which are suitable for diagnostic purposes. When a proprietary fragment or a public database sequence is selected for its specificity and ubiquity, it increases the probability that subsets thereof will also be specific and ubiquitous.

20

The proprietary DNA fragments have been obtained as a repertory of sequences created by amplifying MRSA nucleic acids with new primers. These primers and the repertory of nucleic acids as well as the repertory of nucleotide sequences are further objects of this invention (Tables 4, 5, 6, 7, 8 and 9).

25

Claims therefore are in accordance with the present invention.

SEQUENCES FOR DETECTION AND IDENTIFICATION OF MRSA

In the description of this invention, the terms «nucleic acids» and «sequences»
5 might be used interchangeably. However, «nucleic acids» are chemical entities
while «sequences» are the pieces of information encoded by these «nucleic acids».
Both nucleic acids and sequences are equivalently valuable sources of information
for the matter pertaining to this invention.

10 **Oligonucleotide primers and probes design and synthesis**

As part of the design rules, all oligonucleotides (probes for hybridization and
primers for DNA amplification by PCR) were evaluated for their suitability for
hybridization or PCR amplification by computer analysis using standard programs
15 (i.e. the GCG Wisconsin package programs, the primer analysis software Oligo™
6 and MFOLD 3.0). The potential suitability of the PCR primer pairs was also
evaluated prior to their synthesis by verifying the absence of unwanted features
such as long stretches of one nucleotide and a high proportion of G or C residues at
the 3' end (Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and
20 Applications, American Society for Microbiology, Washington, D.C.).
Oligonucleotide amplification primers were synthesized using an automated DNA
synthesizer (Applied Biosystems). Molecular beacon designs were evaluated using
criteria established by Kramer *et al.* (<http://www.molecular-beacons.org>).

25 The oligonucleotide sequence of primers or probes may be derived from either
strand of the duplex DNA. The primers or probes may consist of the bases A, G, C,
or T or analogs and they may be degenerated at one or more chosen nucleotide
position(s) (Nichols *et al.*, 1994, Nature 369:492-493). Primers and probes may
also consist of nucleotide analogs such as Locked Nucleic Acids (LNA) (Koskinen

al., 1998, Tetrahedron 54:3607-3630), and Peptide Nucleic Acids (PNA) (Egholm *et al.*, 1993, Nature 365:566-568). The primers or probes may be of any suitable length and may be selected anywhere within the DNA sequences from proprietary fragments, or from selected database sequences which are suitable for the detection
5 of MRSA.

Variants for a given target microbial gene are naturally occurring and are attributable to sequence variation within that gene during evolution (Watson *et al.*, 1987, Molecular Biology of the Gene, 4th ed., The Benjamin/Cummings Publishing
10 Company, Menlo Park, CA; Lewin, 1989, Genes IV, John Wiley & Sons, New York, NY). For example, different strains of the same microbial species may have a single or more nucleotide variation(s) at the oligonucleotide hybridization site. The person skilled in the art is well aware of the existence of variant nucleic acids and/or sequences for a specific gene and that the frequency of sequence variations
15 depends on the selective pressure during evolution on a given gene product. The detection of a variant sequence for a region between two PCR primers may be demonstrated by sequencing the amplification product. In order to show the presence of sequence variations at the primer hybridization site, one has to amplify a larger DNA target with PCR primers outside that hybridization site. Sequencing
20 of this larger fragment will allow the detection of sequence variation at this primer hybridization site. A similar strategy may be applied to show variations at the hybridization site of a probe. Insofar as the divergence of the target nucleic acids and/or sequences or a part thereof does not affect significantly the sensitivity and/or specificity and/or ubiquity of the amplification primers or probes, variant
25 microbial DNA is under the scope of this invention. Variants of the selected primers or probes may also be used to amplify or hybridize to a variant target DNA.

DNA amplification

For DNA amplification by the widely used PCR method, primer pairs were derived from our proprietary DNA fragments or from public database sequences.

5

During DNA amplification by PCR, two oligonucleotide primers binding respectively to each strand of the heat-denatured target DNA from the microbial genome are used to amplify exponentially *in vitro* the target DNA by successive thermal cycles allowing denaturation of the DNA, annealing of the primers and
10 synthesis of new targets at each cycle (Persing *et al*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.).

Briefly, the PCR protocols on a standard thermocycler (PTC-200 from MJ
15 Research Inc., Watertown, MA) were as follows: Treated standardized bacterial suspensions or genomic DNA prepared from bacterial cultures or clinical specimens were amplified in a 20 µl PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 2.5 mM MgCl₂, 0.4 µM of each primer, 200 µM of each of the four dNTPs (Pharmacia Biotech), 3.3 µg/µl bovine
20 serum albumin (BSA) (Sigma-Aldrich Canada Ltd, Oakville, Ontario, Canada) and 0.5 unit of *Taq* DNA polymerase (Promega Corp., Madison, WI) combined with the *TaqStart*TM antibody (BD Biosciences, Palo Alto, CA). The *TaqStart*TM antibody, which is a neutralizing monoclonal antibody to *Taq* DNA polymerase, was added to all PCR reactions to enhance the specificity and the sensitivity of the
25 amplifications (Kellogg *et al.*, 1994, Biotechniques 16:1134-1137). The treatment of bacterial cultures or of clinical specimens consists in a rapid protocol to lyse the microbial cells and eliminate or neutralize PCR inhibitors (described in co-pending application US 60/306,163). For amplification from purified genomic DNA, the samples were added directly to the PCR amplification mixture. An internal control,

derived from sequences not found in the target MREJ sequences or in the human genome, was used to verify the efficiency of the PCR reaction and the absence of significant PCR inhibition.

- 5 The number of cycles performed for the PCR assays varies according to the sensitivity level required. For example, the sensitivity level required for microbial detection directly from a clinical specimen is higher than for detection from a microbial culture. Consequently, more sensitive PCR assays having more thermal cycles are probably required for direct detection from clinical specimens.

10

The person skilled in the art of nucleic acid amplification knows the existence of other rapid amplification procedures such as ligase chain reaction (LCR), reverse transcriptase PCR (RT-PCR), transcription-mediated amplification (TMA), self-sustained sequence replication (3SR), nucleic acid sequence-based amplification
15 (NASBA), strand displacement amplification (SDA), branched DNA (bDNA), cycling probe technology (CPT), solid phase amplification (SPA), rolling circle amplification technology (RCA), solid phase RCA, anchored SDA and nuclease dependent signal amplification (NDSA) (Lee *et al.*, 1997, Nucleic Acid Amplification Technologies: Application to Disease Diagnosis, Eaton Publishing,
20 Boston, MA; Persing *et al.*, 1993, Diagnostic Molecular Microbiology: Principles and Applications, American Society for Microbiology, Washington, D.C.; Westin *et al.*, 2000, Nat. Biotechnol. 18:199-204). The scope of this invention is not limited to the use of amplification by PCR, but rather includes the use of any nucleic acid amplification method or any other procedure which may be used to
25 increase the sensitivity and/or the rapidity of nucleic acid-based diagnostic tests. The scope of the present invention also covers the use of any nucleic acids amplification and detection technology including real-time or post-amplification detection technologies, any amplification technology combined with detection, any hybridization nucleic acid chips or array technologies, any amplification chips or

combination of amplification and hybridization chip technologies. Detection and identification by any nucleotide sequencing method is also under the scope of the present invention.

- 5 Any oligonucleotide derived from the *S. aureus* MREJ DNA sequences and used with any nucleic acid amplification and/or hybridization technologies are also under the scope of this invention.

Evaluation of the MRSA detection method developed by Hiramatsu *et al.*

10

According to Hiramatsu *et al.* (Ito *et al.*, 1999, Antimicrob. Agents Chemother. 43:1449-1458; Katayama *et al.*, 2000, Antimicrob. Agents Chemother. 44:1549-1555; Ito *et al.*, 2001, Antimicrob. Agents Chemother. 45:1323-1336, Ma *et al.*, 2002, Antimicrob. Agents Chemother. 46:1147-1152), four types of SCC mec DNA
15 are found among MRSA strains. They have found that SCC mec DNAs are integrated at a specific site of the MSSA chromosome (named *orfX*). They developed a MRSA-specific multiplex PCR assay including primers that can hybridize to the right extremity of SCC mec types I, II and III (SEQ ID NOs.: 18, 19, 20, 21, 22, 23, 24 in US patent 6,156,507 corresponding to SEQ IDNOs.: 52,
20 53, 54, 55, 56, 57, 58, respectively, in the present invention) as well as primers specific to the *S. aureus* chromosome to the right of the SCC mec integration site (SEQ ID NO.: 25, 28, 27, 26, 29 in US patent 6,156,507 corresponding to SEQ ID NOs.: 59, 60, 61, 62, 63, respectively, in the present invention) (Table 1 and Figure 1). The set of primers described by Hiramatsu *et al.* as being the optimal primer
25 combination (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) was used in the present invention to test by PCR a variety of MRSA, MSSA, methicillin-resistant CNS (MRCNS) and methicillin-sensitive CNS (MSCNS) strains (Table 2). A PCR assay performed using a standard thermocycler (PTC-200 from MJ Research Inc.) was

used to test the ubiquity, the specificity and the sensitivity of these primers using the following protocol: one μ l of a treated standardized bacterial suspension or of a genomic DNA preparation purified from bacteria were amplified in a 20 μ l PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of each of the SCCmec- and *S. aureus* chromosome-specific primers (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention), 200 μ M of each of the four dNTPs (Pharmacia Biotech), 3.3 μ g/ μ l BSA (Sigma), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences).

PCR reactions were then subjected to thermal cycling 3 min at 94°C followed by 40 cycles of 60 seconds at 95°C for the denaturation step, 60 seconds at 55°C for the annealing step, and 60 seconds at 72°C for the extension step, then followed by a terminal extension of 7 minutes at 72°C using a standard thermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide. Twenty of the 39 MRSA strains tested were not amplified with the PCR assay developed by Hiramatsu *et al.* (Example 1, Tables 2 and 3).

20

With a view of establishing a rapid diagnostic test for MRSA, the present inventors developed new sets of primers specific to the right extremity of SCCmec types I and II (SEQ ID NOs.: 66, 100 and 101) (Annex 1), SCCmec type II (SEQ ID NOs.: 97 and 99), SCCmec type III (SEQ ID NOs.: 67, 98 and 102) and in the *S. aureus* chromosome to the right of the SCCmec integration site (SEQ ID NOs.: 64, 70, 71, 72, 73, 74, 75 and 76) (Table 5). These primers, amplifying short amplicons (171 to 278 bp), are compatible for use in rapid PCR assays (Table 7). The design of these primers was based on analysis of multiple sequence alignments of *orfX* and SCCmec sequences described by Hiramatsu *et al.* (US patent

6,156,507) or available from GenBank (Table 10, Annex I). These different sets of primers were used to test by PCR a variety of MRSA, MSSA, MRCNS and MSCNS strains. Several amplification primers were developed to detect all three SCCmec types (SEQ ID NOs.: 97 and 99 for SCCmec type II, SEQ ID NOs.: 66, 100 and 101 for SCCmec types I and II and SEQ ID NOs.: 67, 98 and 102 for SCCmec type III). Primers were chosen according to their specificity for MRSA strains, their analytical sensitivity in PCR and the length of the PCR product. A set of two primers was chosen for the SCCmec right extremity region (SEQ ID NO.: 66 specific to SCCmec types I and II; SEQ ID NO.: 67 specific to SCCmec type III). Of the 8 different primers designed to anneal on the *S. aureus* chromosome to the right of the SCCmec integration site (targeting *orfX* gene) (SEQ ID NOs.: 64, 70, 71, 72, 73, 74, 75 and 76), only one (SEQ ID NO.: 64) was found to be specific for MRSA based on testing with a variety of MRSA, MSSA, MRCNS and MSCNS strains (Table 12). Consequently, a PCR assay using the optimal set of primers (SEQ ID NOs.: 64, 66 and 67) which could amplify specifically MRSA strains containing SCCmec types I, II and III was developed (Figure 2, Annex I). While the PCR assay developed with this novel set of primers was highly sensitive (i.e. allowed the detection of 2 to 5 copies of genome for all three SCCmec types) (Table 11), it had the same shortcomings (i.e. lack of ubiquity) of the test developed by Hiramatsu et al. The 20 MRSA strains which were not amplified by the Hiramatsu et al. primers were also not detected by the set of primers comprising SEQ ID NOs.: 64, 66 and 67 (Tables 3 and 12). Clearly, diagnostic tools for achieving at least 50% ubiquity amongst the tested strains are needed.

With a view to establish a more ubiquitous (i.e. ability to detect all or most MRSA strains) detection and identification method for MRSA, we determined the sequence of the MREJ present in these 20 MRSA strains which were not amplified. This research has led to the discovery and identification of seven novel distinct MREJ target sequences which can be used for diagnostic purposes. These

seven new MREJ sequences could not have been predicted nor detected with the system described in US patent 6,156,507 by Hiramatsu *et al.* Namely, the present invention represents an improved method for the detection and identification of MRSA because it provides a more ubiquitous diagnostic method which allows for
5 the detection of all major epidemic MRSA clones from around the world.

Sequencing of MREJ nucleotide sequences from MRSA strains not amplifiable with primers specific to SCCmec types I, II and III

10 Since DNA from twenty MRSA strains were not amplified with the set of primers developed by Hiramatsu *et al.* (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) (Tables 2 and 3) nor with the set of primers developed in the present invention based on the same three SCCmec types (I, II and III) sequences (SEQ ID NOs.: 64,
15 66 and 67) (Table 12), the nucleotide sequence of the MREJ was determined for sixteen of these twenty MRSA strains.

Transposase of IS431 is often associated with the insertion of resistance genes within the *mec* locus. The gene encoding this transposase has been described
20 frequently in one or more copies within the right segment of SCCmec (Oliveira *et al.*, 2000, Antimicrob. Agents Chemother. **44**:1906-1910; Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-36). Therefore, in a first attempt to sequence the novel MREJ for 16 of the 20 MRSA strains described in Table 3, a primer was designed in the sequence of the gene coding for the transposase of
25 IS431 (SEQ ID NO.: 68) and combined with an *orfX*-specific primer to the right of the SCCmec integration site (SEQ ID NO.: 70) (Tables 5 and 8). The strategy used to select these primers is illustrated in Figure 3.

The MREJ fragments to be sequenced were amplified using the following amplification protocol: one μL of treated cell suspension (or of a purified genomic DNA preparation) was transferred directly into 4 tubes containing 39 μL of a PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl_2 , 1 μM of each of the 2 primers (SEQ ID NOs.: 68 and 70), 200 μM of each of the four dNTPs, 3.3 $\mu\text{g}/\mu\text{L}$ of BSA (Sigma-Aldrich Canada Ltd) and 0.5 unit of *Taq* DNA polymerase (Promega) coupled with the *TaqStart*TM Antibody (BD Biosciences). PCR reactions were submitted to cycling using a standard thermocycler (PTC-200 from MJ Research Inc.) as follows: 3 min at 94 °C followed by 40 cycles of 5 sec at 95 °C for the denaturation step, 30 sec at 55 °C for the annealing step and 2 min at 72 °C for the extension step.

Subsequently, the four PCR-amplified mixtures were pooled and 10 μL of the mixture were resolved by electrophoresis in a 1.2% agarose gel containing 0.25 $\mu\text{g}/\text{mL}$ of ethidium bromide. The amplicons were then visualized with an Alpha-Imager (Alpha Innotech Corporation, San Leandro, CA) by exposing to UV light at 254 nm. Amplicon size was estimated by comparison with a 1 kb molecular weight ladder (Life Technologies, Burlington, Ontario, Canada). The remaining PCR-amplified mixture (150 μL , total) was also resolved by electrophoresis in a 1.2% agarose gel. The amplicons were then visualized by staining with methylene blue (Flores *et al.*, 1992, Biotechniques, 13:203-205). Amplicon size was once again estimated by comparison with a 1 kb molecular weight ladder. Of the sixteen strains selected from the twenty described in Table 3, six were amplified using SEQ ID NOs.: 68 and 70 as primers (CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504). For these six MRSA strains, an amplification product of 1.2 kb was obtained. The band corresponding to this specific amplification product was excised from the agarose gel and purified using the QIAquickTM gel extraction kit (QIAGEN Inc., Chatsworth, CA). The gel-

purified DNA fragment was then used directly in the sequencing protocol. Both strands of the MREJ amplification products were sequenced by the dideoxynucleotide chain termination sequencing method by using an Applied Biosystems automated DNA sequencer (model 377) with their Big Dye™ Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems, Foster City, CA). The sequencing reactions were performed by using the same primers (SEQ ID NOs.: 68 and 70) and 10 ng/100 bp per reaction of the gel-purified amplicons. Sequencing of MREJ from the six MRSA strains (CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504) described in Table 3 yielded SEQ ID NOs.: 42, 43, 44, 45, 46 and 51, respectively (Table 4).

In order to ensure that the determined sequence did not contain errors attributable to the sequencing of PCR artefacts, we have sequenced two preparations of the gel-purified MREJ amplification products originating from two independent PCR amplifications. For most target fragments, the sequences determined for both amplicon preparations were identical. Furthermore, the sequences of both strands were 100% complementary thereby confirming the high accuracy of the determined sequence. The MREJ sequences determined using the above strategy are described in the Sequence Listing and in Table 4.

20

In order to sequence MREJ in strains for which no amplicon had been obtained using the strategy including primers specific to the transposase gene of IS431 and *orfX*, another strategy using primers targeting *mecA* and *orfX* sequences was used to amplify longer genomic fragments. A new PCR primer targeting *mecA* (SEQ ID NO.: 69) (Table 8) to be used in combination with the same primer in the *orfX* sequence (SEQ ID NO.: 70). The strategy used to select these primers is illustrated in Figure 3.

25

The following amplification protocol was used: Purified genomic DNA (300 ng) was transferred to a final volume of 50 µl of a PCR reaction mixture. Each PCR reaction contained 1X *Herculase* buffer (Stratagene, La Jolla, CA), 0.8 µM of each of the 2 primers (SEQ ID NOs.: 69 and 70), 0.56 mM of each of the four dNTPs and 5 units of *Herculase* (Stratagene). PCR reactions were subjected to cycling using a standard thermal cycler (PTC-200 from MJ Research Inc.) as follows: 2 min at 92 °C followed by 35 or 40 cycles of 10 sec at 92 °C for the denaturation step, 30 sec at 55 °C for the annealing step and 30 min at 68 °C for the extension step.

10

Subsequently, 10 µL of the PCR-amplified mixture were resolved by electrophoresis in a 0.7% agarose gel containing 0.25 µg/mL of ethidium bromide. The amplicons were then visualized as described above. Amplicon size was estimated by comparison with a 1 kb molecular weight ladder (Life Technologies).

15 A reamplification reaction was then performed in 2 to 5 tubes using the same protocol with 3 µl of the first PCR reaction used as test sample for the second amplification. The PCR-reamplified mixtures were pooled and also resolved by electrophoresis in a 0.7% agarose gel. The amplicons were then visualized by staining with methylene blue as described above. An amplification product of

20 approximately 12 kb was obtained using this amplification strategy for all strains tested. The band corresponding to the specific amplification product was excised from the agarose gel and purified as described above. The gel-purified DNA fragment was then used directly in the sequencing protocol as described above. The sequencing reactions were performed by using the same amplification primers

25 (SEQ ID NOs.: 69 and 70) and 425-495 ng of the gel-purified amplicons per reaction. Subsequently, internal sequencing primers (SEQ ID NOs.: 65, 77 and 96) (Table 8) were used to obtain sequence data on both strands for a larger portion of the amplicon. Five of the 20 MRSA strains (CCRI-1331, CCRI-1263, CCRI-1377, CCRI-1311 and CCRI-2025) described in Table 3 were sequenced using this

strategy, yielding SEQ ID NOs.: 46, 47, 48, 49 and 50, respectively (Table 4). Sequence within *mecA* gene was also obtained from the generated amplicons yielding SEQ ID NOs: 27, 28, 29, 30 and 31 from strains CCRI-2025, CCRI-1263, CCRI-1311, CCRI-1331 and CCRI-1377, respectively (Table 4). Longer
5 sequences within the *mecA* gene and from downstream regions were also obtained for strains CCRI-2025, CCRI-1331, and CCRI-1377 as described below.

In order to obtain longer sequences of the *orfX* gene, two other strategies using primers targeting *mecA* and *orfX* sequences (at the start codon) was used to amplify
10 longer chromosome fragments. A new PCR primer was designed in *orfX* (SEQ ID NO.: 132) to be used in combination with the same primer in the *mecA* gene (SEQ ID NO.: 69). The strategy used to select these primers is illustrated in Figure 3. Eight *S. aureus* strains were amplified using primers SEQ ID NOs.: 69 and 132 (CCRI-9860, CCRI-9208, CCRI-9504, CCRI-1331, CCRI-9583, CCRI-9681,
15 CCRI-2025 and CCRI-1377). The strategy used to select these primers is illustrated in Figure 3.

The following amplification protocol was used: Purified genomic DNA (350 to 500 ng) was transferred to a 50 µl PCR reaction mixture. Each PCR reaction
20 contained 1X Herculase buffer (Stratagene), 0.8 µM of each of the set of 2 primers (SEQ ID NOs.: 69 and 132), 0.56 mM of each of the four dNTPs and 7.5 units of *Herculase* (Stratagene) with 1 mM MgCl₂. PCR reactions were subjected to thermocycling as described above.

25 Subsequently, 5 µL of the PCR-amplified mixture were resolved by electrophoresis in a 0.8% agarose gel containing 0.25 µg/mL of ethidium bromide. The amplicons were then visualized as described above. For one *S. aureus* strain (CCRI-9583), a reamplification was then performed by using primers SEQ ID NOs.: 96 and 158 (Figure 3) in 4 tubes, using the same PCR protocol, with 2 µl of

the first PCR reaction as test sample for the second amplification. The PCR-reamplified mixtures were pooled and also resolved by electrophoresis in a 0.8% agarose gel. The amplicons were then visualized by staining with methylene blue as described above. A band of approximately 12 to 20 kb was obtained using this
5 amplification strategy depending on the strains tested. The band corresponding to the specific amplification product was excised from the agarose gel and purified using the QIAquick™ gel extraction kit or QIAEX II gel extraction kit (QIAGEN Inc.). Two strains, CCRI-9583 and CCRI-9589, were also amplified with primers SEQ ID NOs.: 132 and 150, generating an amplification product of 1.5 kb. Long
10 amplicons (12-20 kb) were sequenced using 0.6 to 1 µg per reaction, while short amplicons (1.5 kb) were sequenced using 150 ng per reaction. Sequencing reactions were performed using different sets of primers for each *S. aureus* strain:
1) SEQ ID NOs.: 68, 70, 132, 145, 146, 147, 156, 157 and 158 for strain CCRI-9504; 2) SEQ ID NOs.: 70, 132, 154 and 155 for strain CCRI-2025; 3) SEQ ID
15 NOs.: 70, 132, 148, 149, 158 and 159 for strain CCRI-9681; 4) SEQ ID NOs.: 70, 132, 187, and 188 for strain CCRI-9860; 5) SEQ ID NOs.: 70, 132, 150 and 159 for strain CCRI-9589, 6) SEQ ID NOs.: 114, 123, 132, 150 and 158 for strain CCRI-9583; 7) SEQ ID NOs.: 70, 132, 154 and 155 for strain CCRI-1377, 8) SEQ ID NOs.: 70, 132, 158 and 159 for strain CCRI-9208; 9) SEQ ID NOs.: 68, 70, 132,
20 145, 146, 147 and 158 for strain CCRI-1331; and 10) SEQ ID NOs.: 126 and 127 for strain CCRI-9770.

In one strain (CCRI-9770), the *orfX* and *orfSA0022* genes were shown to be totally or partially deleted based on amplification using primers specific to these genes
25 (SEQ ID NOs.: 132 and 159 and SEQ ID NOs.: 128 and 129, respectively) (Table 8). Subsequently, a new PCR primer was designed in *orfSA0021* (SEQ ID NO.: 126) to be used in combination with the same primer in the *mecA* gene (SEQ ID NO.: 69). An amplification product of 4.5 kb was obtained with this primer set.

Amplification, purification of amplicons and sequencing of amplicons were performed as described above.

To obtain the sequence of the *SSCmec* region containing *mecA* for ten of the 20
5 MRSA strains described in Table 3 (CCRI-9504, CCRI-2025, CCRI-9208, CCRI-1331, CCRI-9681, CCRI-9860, CCRI-9770, CCRI-9589, CCRI-9583 and CCRI-1377), the primer described above designed in *mecA* (SEQ ID NO.: 69) was used in combination with a primer designed in the downstream region of *mecA* (SEQ ID NO.: 118) (Table 8). An amplification product of 2 kb was obtained for all the
10 strains tested. For one strain, CCRI-9583, a re-amplification with primers SEQ ID NOs.: 96 and 118 was performed with the amplicon generated with primers SEQ ID NOs.: 69 and 132 described above. The amplification, re-amplification, purification of amplicons and sequencing reactions were performed as described above. Sequencing reactions were performed with amplicons generated with SEQ
15 ID NOs.: 69 and 132 described above or SEQ ID NOs.: 69 and 118. Different sets of sequencing primers were used for each *S. aureus* strain: 1) SEQ ID NOs.: 69, 96, 117, 118, 120, 151, 152 for strains CCRI-9504, CCRI-2025, CCRI-1331, CCRI-9770 and CCRI-1377; 2) SEQ ID NOs.: 69, 96, 118 and 120 for strains CCRI-9208, CCRI-9681 and CCRI-9589; 3) SEQ ID NOs.: 69, 96, 117, 118, 120
20 and 152 for strain CCRI-9860; and 4) SEQ ID NOs.: 96, 117, 118, 119, 120, 151 and 152 for strain CCRI-9583.

The sequences obtained for 16 of the 20 strains non-amplifiable by the Hiramatsu assay (Table 4) were then compared to the sequences available from public
25 databases. In all cases, portions of the sequence had an identity close to 100% to publicly available sequences for *orfX* (SEQ ID NOs.: 42-51, 165-168 and 171) or *mecA* and downstream region (SEQ ID NOs.: 27-31, 189-193, 195, 197-199 and 225). However, while the *orfX* portion of the fragments (SEQ ID NOs.: 42-51, 165-168 and 171) shared nearly 100% identity with the *orfX* gene of MSSA strain

NCTC 8325 described by Hiramatsu *et al.* (SEQ ID NO.: 3), the DNA sequence within the right extremity of SCCmec itself was shown to be very different from those of types I, II, III and IV described by Hiramatsu *et al.* (Table 13, Figure 4). Six different novel sequence types were obtained.

5

It should be noted that Hiramatsu *et al.* demonstrated that SCCmec type I could be associated with MREP type i, SCCmec types II and IV are associated with MREP type ii, and SCCmec type III is associated with MREP type iii. Our MREJ sequencing data from various MRSA strains led to the discovery of 6 novel MREP
10 types designated types iv, v, vi, vii, viii, and ix. The MREJ comprising distinct MREP types were named according to the MREP numbering scheme. Hence, MREP type i is comprised within MREJ type i, MREP type ii is comprised within MREJ type ii and so on up to MREP type ix.

15 The sequences within the right extremity of SCCmec obtained from strains CCRI-178, CCRI-8895, CCRI-8903, CCRI-1324, CCRI-1331 and CCRI-9504 (SEQ ID NOs.: 42, 43, 44, 45, 46 and 51) were nearly identical to each other and exhibited nearly 100% identity with IS431 (GenBank accession numbers AF422691, ABO37671, AF411934). However, our sequence data revealed for the first time
20 the location of this IS431 sequence at the right extremity of SCCmec adjacent to the integration site. Therefore, as the sequences at the right extremity of SCCmec from these 6 MRSA strains were different from those of SCCmec type I from strain NCTC 10442, SCCmec type II from strain N315, SCCmec type III from strain 85/2082 and SCCmec type IV from strains CA05 and 8/6-3P described by
25 Hiramatsu *et al.* (Ito *et al.*, 2001, Antimicrob. Agents Chemother. **45**:1323-1336; Ma *et al.*, 2002, Antimicrob. Agents Chemother. **46**:1147-1152), these new sequences were designated as MREP type iv (SEQ ID NOs.: 42-46 and 51). A BLAST search with the SCCmec portion of MREP type iv sequences produced significant alignments with sequences coding for portions of a variety of known

transposases. For example, when compared to Genbank accession no. AB037671, MREP type iv from SEQ ID NO. 51 shared 98% identity with the putative transposase of IS431 and its downstream region; two gaps of 7 nucleotides each were also present in the alignment.

5 Sequences obtained from strains CCRI-1263, CCRI-1377, CCRI-1311 and CCRI-2025 (SEQ ID NOs.: 47-50) were nearly identical to each other and different from all three SCC*mec* types and MREP type iv and, consequently, were designated as MREP type v. When compared with Genbank sequences using BLAST, MREP type v sequences did not share any significant homology with any published
10 sequence, except for the first 28 nucleotides. That short stretch corresponded to the last 11 coding nucleotides of *orfX*, followed by the 17 nucleotides downstream, including the right inverted repeat (IR-R) of SCC*mec*.

Sequence obtained from strain CCRI-9208 was also different from all three SCC*mec* types and MREP types iv and v and, consequently, was designated as
15 MREP type vi (SEQ ID NO.: 171). Upon a BLAST search, MREP type vi was shown to be unique, exhibiting no significant homology to any published sequence.

Sequences obtained from strains CCRI-9583 and CCRI-9589 were also different from all three SCC*mec* types and MREP types iv to vi and were therefore
20 designated as MREP type vii (SEQ ID NOs.: 165 and 166). Upon a BLAST search, MREP type vii was also shown to be unique, exhibiting no significant homology to any published sequence.

Sequence obtained from strain CCRI-9860 was also different from all three SCC*mec* types and MREP types iv to vii and was therefore designated as MREP
25 type viii (SEQ ID NO.: 167). Sequence obtained from strain CCRI-9681 was also different from all three SCC*mec* types and MREP types iv to viii and was therefore designated as MREP type ix (SEQ ID NO.: 168). BLAST searches with the SCC*mec* portion of MREP types viii and ix sequences yielded significant alignments, but only for the first ~150 nucleotides of each MREP type. For

example, the beginning of the MREP type viii sequence had 88% identity with a portion of Genbank accession no. AB063173, but no significant homology with any published sequence was found for the rest of the sequence. In the same manner, the first ~150 nucleotides of MREP type ix had 97% identity with the same portion of AB063173, with the rest of the sequence being unique. The short homologous portion of MREP types viii and ix corresponds in AB063173 to the last 14 coding nucleotides of *orfX*, the IR-R of *SCCmec*, and a portion of *orfCM009*. Although sharing resemblances, MREP types viii and ix are very different from one another; as shown in Table 13, there is only 55.2% identity between both types for the first 500 nucleotides of the *SCCmec* portion.

Finally, we did not obtain any sequence within *SCCmec* from strain CCRI-9770. However, as described in the section "Sequencing of MREJ nucleotide sequences from MRSA strains not amplifiable with primers specific to *SCCmec* types I, II and III", this strain has apparently a partial or total deletion of the *orfX* and *orfSA0022* genes in the chromosomal DNA to the right of the *SCCmec* integration site and this would represent a new right extremity junction. We therefore designated this novel sequence as MREP type x (SEQ ID NO.: 172). Future sequencing should reveal whether this so called MREJ type x contains a novel MREP type x or if the lack of amplification is indeed caused by variation in the chromosomal part of the MREJ.

The sequences of the first 500-nucleotide portion of the right extremity of all *SCCmec* obtained in the present invention were compared to those of *SCCmec* types I, II and III using GCG programs Pileup and Gap. Table 13 depicts the identities at the nucleotide level between *SCCmec* right extremities of the six novel sequences with those of *SCCmec* types I, II and III using the GCG program Gap. While *SCCmec* types I and II showed nearly 79.2% identity (differing only by a 102 bp insertion present in *SCCmec* type II) (Figures 1, 2 and 4), all other MREP types showed identities varying from 40.9 to 57.1%. This explains why the right

extremities of the novel MREP types iv to ix disclosed in the present invention could not have been predicted nor detected with the system described by Hiramatsu *et al.*

- 5 Four strains (CCRI-1312, CCRI-1325, CCRI-9773 and CCRI-9774) described in Table 3 were not sequenced but rather characterized using PCR primers. Strains CCRI-1312 and CCRI-1325 were shown to contain MREP type v using specific amplification primers described in Examples 4, 5 and 6 while strains CCRI-9773 and CCRI-9774 were shown to contain MREP type vii using specific amplification
10 primers described in Example 7.

To obtain the complete sequence of the SCC*mec* present in the MRSA strains described in the present invention, primers targeting the *S. aureus* chromosome to the left (upstream of the *mecA* gene) of the SCC*mec* integration site were
15 developed. Based on available public database sequences, 5 different primers were designed (SEQ ID NOs.: 85-89) (Table 9). These primers can be used in combination with *S. aureus* chromosome-specific primers in order to sequence the entire SCC*mec* or, alternatively, used in combination with a *mecA*-specific primer (SEQ ID NO.: 81) in order to sequence the left extremity junction of SCC*mec*. We
20 have also developed several primers specific to known SCC*mec* sequences spread along the locus in order to obtain the complete sequence of SCC*mec* (Table 9). These primers will allow to assign a SCC*mec* type to the MRSA strains described in the present invention.

25 **Selection of amplification primers from SCC*mec*/orfX sequences**

The MREJ sequences determined by the inventors or selected from public databases were used to select PCR primers for detection and identification of

MRSA. The strategy used to select these PCR primers was based on the analysis of multiple sequence alignments of various MREJ sequences.

Upon analysis of the six new MREP types iv to ix sequence data described above,
5 primers specific to each new MREP type sequence (SEQ ID NOs.: 79, 80, 109, 112, 113, 115, 116 and 204) were designed (Figure 2, Table 5, Examples 3, 4, 5, 6, 7 and 8). Primers specific to MREP types iv, v and vii (SEQ ID NOs.: 79, 80 and 112) were used in multiplex with the three primers to detect SCCmec types I, II and III (SEQ ID NOs: 64, 66 and 67) and the primer specific to the *S. aureus orfX*
10 (SEQ ID NO. 64) (Examples 3, 4, 5, 6 and 7). Primers specific to MREP types vi, viii and ix (SEQ ID NOs.: 204, 115, 116 and 109) were also designed and tested against their specific target (Example 8).

Detection of amplification products

15

Classically, the detection of PCR amplification products is performed by standard ethidium bromide-stained agarose gel electrophoresis as described above. It is however clear that other methods for the detection of specific amplification products, which may be faster and more practical for routine diagnosis, may be
20 used. Examples of such methods are described in co-pending patent application WO01/23604 A2.

Amplicon detection may also be performed by solid support or liquid hybridization using species-specific internal DNA probes hybridizing to an amplification
25 product. Such probes may be generated from any sequence from our repertory and designed to specifically hybridize to DNA amplification products which are objects of the present invention. Alternatively, amplicons can be characterized by sequencing. See co-pending patent application WO01/23604 A2 for examples of detection and sequencing methods.

In order to improve nucleic acid amplification efficiency, the composition of the reaction mixture may be modified (Chakrabarti and Schutt, 2002, *Biotechniques*, 32:866-874; Al-Soud and Radstrom, 2002, *J. Clin. Microbiol.*, 38:4463-4470; Al-Soud and Radstrom, 1998, *Appl. Environ. Microbiol.*, 64:3748-3753; Wilson, 1997, *Appl. Environ. Microbiol.*, 63:3741-3751). Such modifications of the amplification reaction mixture include the use of various polymerases or the addition of nucleic acid amplification facilitators such as betaine, BSA, sulfoxides, protein gp32, detergents, cations, tetramethylammonium chloride and others.

10

In a preferred embodiment, real-time detection of PCR amplification was monitored using molecular beacon probes in a SmartCycler[®] apparatus (Cepheid, Sunnyvale, CA). A multiplex PCR assay containing primers specific to MREP types i to v and *orfX* of *S. aureus* (SEQ ID NOs.: 64, 66, 67, 79 and 80), a molecular beacon probe specific to the *orfX* sequence (SEQ ID NO. 84, see Annex II and Figure 2) and an internal control to monitor PCR inhibition was developed. The internal control contains sequences complementary to MREP type iv- and *orfX*-specific primers (SEQ ID NOs. 79 and 64). The assay also contains a molecular beacon probe labeled with tetrachloro-6-carboxyfluorescein (TET) specific to sequence within DNA fragment generated during amplification of the internal control. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.8 μM of each of the MREP-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 μM of each of the MREP-specific primers (SEQ ID NOs.: 79 and 80), 80 copies of the internal control, 0.2 μM of the TET-labeled molecular beacon probe specific to the internal control, 0.2 μM of the molecular beacon probe (SEQ ID NO.: 84) labeled with 6-carboxyfluorescein (FAM), 330 μM of each of the four dNTPs (Pharmacia Biotech), 3.45 μg/μl of BSA (Sigma), and 0.875 U *Taq* polymerase (Promega) coupled with *TaqStart*[™] Antibody (BD Biosciences). The PCR

amplification on the Smart Cycler[®] was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. Sensitivity tests performed by using
5 purified genomic DNA from one MRSA strain of each MREP type (i to v) showed a detection limit of 2 to 10 genome copies (Example 5). None of the 26 MRCNS or 10 MSCNS tested were positive with this multiplex assay. The eight MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860, CCRI-9583, CCRI-9773, CCRI-9774, CCRI-9589) which harbor the new MREP types vi, viii, ix and x
10 sequences described in the present invention remained undetectable (Example 5).

In a preferred embodiment, detection of MRSA using the real-time multiplex PCR assay on the Smart Cycler[®] apparatus (Cepheid, Sunnyvale, CA) directly from clinical specimens was evaluated. A total of 142 nasal swabs were collected during
15 a MRSA hospital surveillance program at the Montreal General Hospital (Montreal, Quebec, Canada). The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, the swabs were plated onto mannitol agar and then the nasal material from the same swab was prepared with a simple and rapid specimen preparation
20 protocol described in co-pending patent application number US 60/306,163. Classical identification of MRSA was performed by standard culture methods.

The PCR assay detected 33 of the 34 samples positive for MRSA based on the culture method. As compared to culture, the PCR assay detected 8 additional
25 MRSA positive specimens for a sensitivity of 97.1 % and a specificity of 92.6 % (Example 6). This multiplex PCR assay represents a rapid and powerful method for the specific detection of MRSA carriers directly from nasal specimens and can be used with any types of clinical specimens such as wounds, blood or blood culture, CSF, etc.

In a preferred embodiment, a multiplex PCR assay containing primers specific to MREP types i, ii, iii, iv, v and vi and orfX of *S. aureus* (SEQ ID NOs.: 66, 67, 79, 80 and 112), and three molecular beacons probes specific to orfX sequence which allowed detection of the two sequence polymorphisms identified in this region of the orfX sequence was developed. Four of the strains which were not detected with the multiplex assay for the detection of MREP types i to v were now detected with this multiplex assay while the four MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860) which harbor the MREP types vi, viii, ix and x described in the present invention remained undetectable (Example 7). Primers specific to MREP types vi, viii and ix (SEQ ID NOs.: 204, 115, 116 and 109) were also designed and were shown to detect their specific target strains (Example 8). While the primers and probes derived from the teaching of Hiramatsu *et al.*, permitted the detection of only 48.7% (19 strains out of 39) of the MRSA strains of Table 2, the primers and probes derived from the present invention enable the detection of 97.4 % of the strains (38 strains out of 39) (see examples 7 and 8). Therefore it can be said that our assay has a ubiquity superior to 50% for the MRSA strains listed in Table 2.

Specificity, ubiquity and sensitivity tests for oligonucleotide primers and probes

The specificity of oligonucleotide primers and probes was tested by amplification of DNA or by hybridization with staphylococcal species. All of the staphylococcal species tested were likely to be pathogens associated with infections or potential contaminants which can be isolated from clinical specimens. Each target DNA could be released from microbial cells using standard chemical and/or physical treatments to lyse the cells (Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) or alternatively, genomic DNA purified with the GNOME™ DNA kit (Qbiogene, Carlsbad, CA) was used. Subsequently, the DNA was subjected to

amplification with the set of primers. Specific primers or probes hybridized only to the target DNA.

Oligonucleotides primers found to amplify specifically DNA from the target
5 MRSA were subsequently tested for their ubiquity by amplification (i.e. ubiquitous primers amplified efficiently most or all isolates of MRSA). Finally, the analytical sensitivity of the PCR assays was determined by using 10-fold or 2-fold dilutions of purified genomic DNA from the targeted microorganisms. For most assays, sensitivity levels in the range of 2-10 genome copies were obtained. The
10 specificity, ubiquity and analytical sensitivity of the PCR assays were tested either directly with bacterial cultures or with purified bacterial genomic DNA.

Molecular beacon probes were tested using the Smart Cycler® platform as described above. A molecular beacon probe was considered specific only when it
15 hybridized solely to DNA amplified from the MREJ of *S. aureus*. Molecular beacon probes found to be specific were subsequently tested for their ubiquity (i.e. ubiquitous probes detected efficiently most or all isolates of the MRSA) by hybridization to bacterial DNAs from various MRSA strains.

20 ***Bacterial strains***

The reference strains used to build proprietary *SCCmec*-chromosome right extremity junction sequence data subrepertories, as well as to test the amplification and hybridization assays, were obtained from (i) the American Type Culture
25 Collection (ATCC), (ii) the Laboratoire de santé publique du Québec (LSPQ) (Ste-Anne de Bellevue, Québec, Canada), (iii) the Centers for Disease Control and Prevention (CDC) (Atlanta, GA), (iv) the Institut Pasteur (Paris, France), and V) the Harmony Collection (London, United Kingdom) (Table 14). Clinical isolates of MRSA, MSSA, MRCNS and MSCNS from various geographical areas were also

used in this invention (Table 15). The identity of our MRSA strains was confirmed by phenotypic testing and reconfirmed by PCR analysis using *S. aureus*-specific primers and *mecA*-specific primers (SEQ ID NOs.: 69 and 81) (Martineau *et al.*, 2000, Antimicrob. Agents Chemother. 44:231-238).

5

For sake of clarity, below is a list of the Examples, Tables, Figures and Annexes of this invention.

DESCRIPTION OF THE EXAMPLES

10

Example 1: Primers developed by Hiramatsu *et al.* can only detect MRSA strains belonging to MREP types i, ii, and iii while missing prevalent novel MREP types.

Example 2: Detection and identification of MRSA using primers specific to MREP types i, ii and iii sequences developed in the present invention.

15 **Example 3:** Development of a multiplex PCR assay on a standard thermocycler for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences.

Example 4: Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv
20 and v sequences.

Example 5: Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences and including an internal control.

Example 6: Detection of MRSA using the real-time multiplex assay on the Smart
25 Cycler® based on MREP types i, ii, iii, iv and v sequences for the detection of MRSA directly from clinical specimens.

Example 7: Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv, v, vi and vii sequences.

Example 8: Developement of real-time PCR assays on the Smart Cycler[®] for detection and identification of MRSA based on MREP types vi, viii and ix.

DESCRIPTION OF THE TABLES

5

Table 1 provides information about all PCR primers developed by Hiramatsu *et al.* in US patent 6,156,507.

Table 2 is a compilation of results (ubiquity and specificity) for the detection of SCC*mec-orfX* right extremity junction using primers described by Hiramatsu *et al.*
10 in US patent 6,156,507 on a standard thermocycler.

Table 3 is a list of MRSA strains not amplifiable using primers targeting types I, II and III of SCC*mec-orfX* right extremity junction sequences.

Table 4 is a list of novel sequences revealed in the present invention.

Table 5 provides information about all primers developed in the present invention.

15 **Table 6** is a list of molecular beacon probes developed in the present invention.

Table 7 shows amplicon sizes of the different primer pairs described by Hiramatsu *et al.* in US patent 6,156,507 or developed in the present invention.

Table 8 provides information about primers developed in the present invention to sequence the SCC*mec*-chromosome right extremity junction.

20 **Table 9** provides information about primers developed in the present invention to obtain sequence of the complete SCC*mec*.

Table 10 is a list of the sequences available from public databases (GenBank, genome projects or US patent 6,156,507) used in the present invention to design primers and probes.

25 **Table 11** gives analytical sensitivity of the PCR assay developed in the present invention using primers targeting types I, II and III of SCC*mec-orfX* right extremity junction sequences and performed using a standard thermocycler.

Table 12 is a compilation of results (ubiquity and specificity) for the detection of MRSA using primers developed in the present invention which target types I, II

and III of *SCCmec-orfX* right extremity junction sequences and performed using a standard thermocycler.

Table 13 shows a comparison of sequence identities between the first 500 nucleotides of *SCCmec* right extremities between 9 types of MREP.

5 **Table 14** provides information about the reference strains of MRSA, MSSA, MRCNS and MSCNS used to validate the PCR assays developed in the present invention.

Table 15 provides information about the origin of clinical strains of MRSA, MSSA, MRCNS and MSCNS used to validate the PCR assays described in the
10 present invention.

Table 16 depicts the analytical sensitivity of the PCR assay developed in the present invention using primers targeting 5 types of MREP sequences and performed on a standard thermocycler.

Table 17 is a compilation of results (ubiquity and specificity) for the PCR assay
15 developed in the present invention using primers targeting 5 types of MREP sequences and performed on a standard thermocycler.

Table 18 depicts the analytical sensitivity of the PCR assay developed in the present invention using the SmartCycler[®] platform for the detection of 5 types of MREP.

20 **Table 19** is a compilation of results (ubiquity and specificity) for the PCR assay developed in the present invention using primers and a molecular beacon probe targeting 5 types of MREP sequences and performed on the Smart Cycler[®] platform.

Table 20 depicts the analytical sensitivity of the PCR assay developed in the
25 present invention using the SmartCycler[®] platform for the detection of 6 MREP types.

Table 21 is a compilation of results (ubiquity and specificity) for the PCR assay developed in the present invention using primers and a molecular beacon probe

targeting 6 types of MREP sequences and performed on the Smart Cyclor[®] platform.

DESCRIPTION OF THE FIGURES

5

Figure 1 is a diagram illustrating the position of the primers developed by Hiramatsu *et al.* (US patent 6,156,507) in the SCC*mec*-chromosome right extremity junction for detection and identification of MRSA.

10 **Figure 2** is a diagram illustrating the position of the primers selected in the present invention in the SCC*mec-orfX* right extremity junction for detection and identification of MRSA.

Figure 3 is a diagram illustrating the position of the primers selected in the present invention to sequence new MREP types.

Figure 4 illustrates a sequence alignment of nine MREP types.

15

FIGURE LEGENDS

Figure 1. Schematic organization of types I, II and III SCC*mec-orfX* right extremity junctions and localization of the primers (SEQ ID NOs: 52-63) described by Hiramatsu *et al.* for the detection and identification of MRSA. Amplicon sizes are depicted in Table 7.

20 **Figure 2.** Schematic organization of MREP types i, ii, iii, iv, v, vi, vii, viii and ix and localization of the primers and molecular beacon targeting all MREP types (SEQ ID NOs. 20, 64, 66, 67, 79, 80, 84, 112, 115, 116, 84, 163 and 164) which were developed in the present invention. Amplicon sizes are depicted in Table 7.

25 **Figure 3.** Schematic organization of the SCC*mec*-chromosome right extremity junctions and localization of the primers (SEQ IDNOs. 65, 68, 69, 70, 77, 96, 118, 126, 132, 150 and 158) developed in the present invention for the sequencing of MREP types iv, v, vi, vii, viii, ix and x.

Figure 4. Multiple sequence alignment of representatives of nine MREP types (represented by portions of SEQ IDNOs.: 1, 2, 104, 51, 50, 171, 165, 167 and 168 for types i, ii, iii, iv, v, vi, vii, viii and ix, respectively).

5 DESCRIPTION OF THE ANNEXES

The Annexes show the strategies used for the selection of primers and internal probes:

Annex I illustrates the strategy for the selection of primers from *SCCmec* and *orfX* sequences specific for *SCCmec* types I and II.

Annex II illustrates the strategy for the selection of specific molecular beacon probes for the real-time detection of *SCCmec-orfX* right extremity junctions.

As shown in these Annexes, the selected amplification primers may contain inosines and/or base ambiguities. Inosine is a nucleotide analog able to specifically bind to any of the four nucleotides A, C, G or T. Alternatively, degenerated oligonucleotides which consist of an oligonucleotide mix having two or more of the four nucleotides A, C, G or T at the site of mismatches were used. The inclusion of inosine and/or of degeneracies in the amplification primers allows mismatch tolerance thereby permitting the amplification of a wider array of target nucleotide sequences (Dieffenbach and Dveksler, 1995, PCR Primer: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Plainview, New York).

25

EXAMPLES

EXAMPLE 1:

Primers developed by Hiramatsu *et al.* can only detect MRSA strains belonging to MREP types i, ii, and iii while missing prevalent novel MREP types.

As shown in Figure 1, Hiramatsu *et al.* have developed various primers that can specifically hybridize to the right extremities of types I, II and III SCCmec DNAs. They combined these primers with primers specific to the *S. aureus* chromosome region located to the right of the SCCmec integration site for the detection of MRSA. The primer set (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) was shown by Hiramatsu *et al.* to be the most specific and ubiquitous for detection of MRSA. This set of primers gives amplification products of 1.5 kb for SCCmec type I, 1.6 kb for SCCmec type II and 1.0 kb for SCCmec type III (Table 7). The ubiquity and specificity of this multiplex PCR assay was tested on 39 MRSA strains, 41 MSSA strains, 9 MRCNS strains and 11 MSCNS strains (Table 2). One μ L of a treated standardized bacterial suspension or of a bacterial genomic DNA preparation purified from bacteria were amplified in a 20 μ l PCR reaction mixture. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 2.5 mM MgCl₂, 0.4 μ M of each of the SCCmec- and *orfX*-specific primers (SEQ ID NOs.: 56, 58 and 60), 200 μ M of each of the four dNTPs (Pharmacia Biotech), 3.3 μ g/ μ l of BSA (Sigma), and 0.5 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences).

PCR reactions were then subjected to thermal cycling: 3 min at 94°C followed by 40 cycles of 60 seconds at 95°C for the denaturation step, 60 seconds at 55°C for the annealing step, and 60 seconds at 72°C for the extension step, then followed by a terminal extension of 7 minutes at 72°C using a standard thermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made by electrophoresis in agarose gels (2 %) containing 0.25 μ g/ml of ethidium bromide.

None of the MRCNS or MSCNS strains tested were detected with the set of primers detecting SCCmec types I, II and III. Twenty of the 39 MRSA strains tested were not detected with this multiplex PCR assay (Tables 2 and 3). One of these undetected MRSA strains corresponds to the highly epidemic MRSA
5 Portuguese clone (strain CCRI-9504; De Lencastre *et al.*, 1994. Eur. J. Clin. Microbiol. Infect. Dis. 13:64-73) and another corresponds to the highly epidemic MRSA Canadian clone CMRSA1 (strain CCRI-9589; Simor *et al.* CCDC 1999, 25-12, June 15). These data demonstrate that the primer set developed by Hiramatsu *et al.* (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507
10 corresponding to SEQ ID NOs.: 56, 58 and 60 in the present invention) is not ubiquitous for the detection of MRSA and suggest that some MRSA strains have sequences at the SCCmec right extremity junction which are different from those identified by Hiramatsu *et al.* other types of SCCmec sequences or other sequences at the right extremity of SCCmec (MREP type) are found in MRSA. A limitation
15 of this assay is the non-specific detection of 13 MSSA strains (Table 2).

EXAMPLE 2:

Detection and identification of MRSA using primers specific to MREP types i, ii and iii sequences developed in the present invention. Based on analysis of
20 multiple sequence alignments of *orfX* and SCCmec sequences described by Hiramatsu *et al.* or available from GenBank, a set of primers (SEQ ID NOs: 64, 66, 67) capable of amplifying short segments of types I, II and III of SCCmec-*orfX* right extremity junctions from MRSA strains and discriminating from MRCNS
25 (Annex I and Figure 2) were designed. The chosen set of primers gives amplification products of 176 bp for SCCmec type I, 278 pb for SCCmec type II and 223 bp for SCCmec type III and allows rapid PCR amplification. These primers were used in multiplex PCR to test their ubiquity and specificity using 208 MRSA strains, 252 MSSA strains, 41 MRCNS strains and 21 MRCNS strains

(Table 12). The PCR amplification and detection was performed as described in Example 1. PCR reactions were then subjected to thermal cycling (3 minutes at 94°C followed by 30 or 40 cycles of 1 second at 95°C for the denaturation step and 30 seconds at 60°C for the annealing-extension step, and then followed by a terminal extension of 2 minutes at 72°C) using a standard thermocycler (PTC-200 from MJ Research Inc.). Detection of the PCR products was made as described in Example 1.

None of the MRCNS or MSCNS strains tested were detected with this set of primers (Table 12). However, the twenty MRSA strains which were not detected with the primer set developed by Hiramatsu *et al.* (SEQ ID NOs: 56, 58 and 60) were also not detected with the primers developed in the present invention (Tables 3 and 12). These data also demonstrate that some MRSA strains have sequences at the SCC*mec*-chromosome right extremity junction which are different from those identified by Hiramatsu *et al.* Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 12). The clinical significance of this finding remains to be established since these apparent MSSA strains could be the result of a recent deletion in the *mec* locus (Deplano *et al.*, 2000, J. Antimicrob. Chemotherapy, 46:617-619; Inglis *et al.*, 1990, J. Gen. Microbiol., 136:2231-2239; Inglis *et al.*, 1993, J. Infect. Dis., 167:323-328; Lawrence *et al.* 1996, J. Hosp. Infect., 33:49-53; Wada *et al.*, 1991, Biochem. Biophys. Res. Comm., 176:1319-1326).

EXAMPLE 3:

25

Development of a multiplex PCR assay on a standard thermocycler for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences. Upon analysis of two of the new MREP types iv and v sequence data described in the present invention, two new primers (SEQ ID NOs.: 79 and 80)

were designed and used in multiplex with the three primers SEQ IDNOs.: 64, 66 and 67 described in Example 2. PCR amplification and detection of the PCR products was performed as described in Example 2. Sensitivity tests performed by using ten-fold or two-fold dilutions of purified genomic DNA from various MRSA strains of each MREP type showed a detection limit of 5 to 10 genome copies (Table 16). Specificity tests were performed using 0,1 ng of purified genomic DNA or 1 µl of a standardized bacterial suspension. All MRCNS or MSCNS strains tested were negative with this multiplex assay (Table 17). Twelve of the 20 MRSA strains which were not detected with the multiplex PCR described in Examples 1 and 2 were now detected with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 12). The eight MRSA strains (CCRI-9208, CCRI-9583, CCRI-9773, CCRI-9774, CCRI-9589, CCRI-9860, CCRI-9681, CCRI-9770) and which harbor the new MREP types vi, vii, viii, ix and x sequences described in the present invention remained undetectable.

EXAMPLE 4:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences. The multiplex PCR assay described in Example 3 containing primers (SEQ ID NOs.: 64, 66, 67, 79 and 80) was adapted to the SmartCycler® platform (Cepheid). A molecular beacon probe specific to the *orfX* sequence was developed (SEQ ID NO. 84, see Annex II). Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.5 mM MgCl₂, 0.4 µM of each of the SCC*mec*- and *orfX*-specific primers (SEQ ID NOs.: 64, 66, 67, 79 and 80), 0.2 µM of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 200 µM of each of the four dNTPs, 3.3 µg/µl of BSA, and 0.5 U *Taq* polymerase coupled with *TaqStart*TM Antibody. The PCR amplification on the Smart Cycler® was performed

as follows: 3 min. at 94°C for initial denaturation, then forty-five cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 59°C for the annealing step and 10 seconds at 72°C for the extension step. Fluorescence detection was performed at the end of each annealing step. Sensitivity tests performed by using purified genomic DNA from several MRSA strains of each MREP type showed a detection limit of 2 to 10 genome copies (Table 18). None of the MRCNS or MSCNS were positive with this multiplex assay (Table 19). Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically. Twelve of the twenty MRSA strains which were not detected with the multiplex PCR described in Examples 1 and 2 were detected by this multiplex assay. As described in Example 3, the eight MRSA strains which harbor the new MREP types vi, vii, viii, ix and x sequences described in the present invention remained undetectable.

15 EXAMPLE 5:

Development of a real-time multiplex PCR assay on the Smart Cycler® for detection and identification of MRSA based on MREP types i, ii, iii, iv and v sequences including an internal control. The multiplex PCR assay described in Example 4 containing primers specific to MREP types i to v and *orfX* of *S. aureus* (SEQ ID NOs.: 64, 66, 67, 79 and 80) and a molecular beacon probe specific to the *orfX* sequence (SEQ ID NO. 84, see Annex II) was optimized to include an internal control to monitor PCR inhibition. This internal control contains sequences complementary to MREP type iv- and *orfX*-specific primers (SEQ ID NOs. 79 and 25 and 64). The assay also contains a TET-labeled molecular beacon probe specific to sequence within the amplicon generated by amplification of the internal control. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.8 µM of each of the MREP-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 µM of each of

the MREP-specific primers (SEQ ID NOs.: 79 and 80), 80 copies of the internal control, 0.2 μ M of the TET-labeled molecular beacon probe specific to the internal control, 0.2 μ M of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 330 μ M of each of the four dNTPs (Pharmacia Biotech), 3.45 μ g/ μ l of BSA
5 (Sigma), and 0.875 U *Taq* polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences). The PCR amplification on the Smart Cycler[®] was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension
10 step. Sensitivity tests performed by using purified genomic DNA from one MRSA strain of each MREP type (i to v) showed a detection limit of 2 to 10 genome copies. None of the 26 MRCNS or 10 MSCNS were positive with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically. As described in Examples 3 and 4, the eight MRSA
15 strains which harbor the new MREP types vi to x sequences described in the present invention remained undetectable.

EXAMPLE 6:

20 Detection of MRSA using the real-time multiplex assay on the Smart Cycler[®] based on MREP types i, ii, iii, iv and v sequences directly from clinical specimens. The assay described in Example 5 was adapted for detection directly from clinical specimens. A total of 142 nasal swabs collected during a MRSA hospital surveillance program at the Montreal General Hospital (Montreal, Quebec,
25 Canada) were tested. The swab samples were tested at the Centre de Recherche en Infectiologie de l'Université Laval within 24 hours of collection. Upon receipt, the swabs were plated onto mannitol agar and then the nasal material from the same swab was prepared with a simple and rapid specimen preparation protocol

described in co-pending patent application number US 60/306,163. Classical identification of MRSA was performed by standard culture methods.

The PCR assay described in Example 5 detected 33 of the 34 samples positive for MRSA based on the culture method. As compared to culture, the PCR assay detected 8 additional MRSA positive specimens for a sensitivity of 97.1 % and a specificity of 92.6 %. This multiplex PCR assay represents a rapid and powerful method for the specific detection of MRSA carriers directly from nasal specimens and can be used with any type of clinical specimens such as wounds, blood or blood culture, CSF, etc.

EXAMPLE 7:

Development of a real-time multiplex PCR assay on the Smart Cycler[®] for detection and identification of MRSA based on MREP types i, ii, iii, iv, v and vii sequences. Upon analysis of the new MREP type vii sequence data described in the present invention (SEQ ID NOs.: 165 and 166), two new primers (SEQ ID NOs.: 112 and 113) were designed and tested in multiplex with the three primers SEQ ID NOs.: 64, 66 and 67 described in Example 2. Primer SEQ ID NO.: 112 was selected for use in the multiplex based on its sensitivity. Three molecular beacon probes specific to the *orfX* sequence which allowed detection of two sequence polymorphisms identified in this region of the *orfX* sequence, based on analysis of SEQ ID NOs.: 173-186, were also used in the multiplex (SEQ ID NOs.: 84, 163 and 164). Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.8 μM of each of the SCC*mec*-specific primers (SEQ ID NOs.: 66 and 67) and *orfX*-specific primer (SEQ ID NO.: 64), 0.4 μM of each of the SCC*mec*-specific primers (SEQ ID NOs.: 79 and 80), 0.2 μM of the FAM-labeled molecular beacon probe (SEQ ID NO.: 84), 330 μM of each of the four dNTPs (Pharmacia Biotech), 3.45 μg/μl of BSA (Sigma), and 0.875 U of

Taq polymerase (Promega) coupled with *TaqStart*TM Antibody (BD Biosciences). The PCR amplification on the Smart Cycler[®] was performed as follows: 3 min. at 95°C for initial denaturation, then forty-eight cycles of three steps consisting of 5 seconds at 95°C for the denaturation step, 15 seconds at 60°C for the annealing step and 15 seconds at 72°C for the extension step. The detection of fluorescence was done at the end of each annealing step. Sensitivity tests performed by using purified genomic DNA from several MRSA strains of each MREP type showed a detection limit of 2 genome copies (Table 20). None of the 26 MRCNS or 8 MSCNS were positive with this multiplex assay. Again, as observed with the Hiramatsu primers, 13 MSSA strains were also detected non-specifically (Table 21). Four of the strains which were not detected with the multiplex assay for the detection of MREP types i to v were now detected with this multiplex assay while the four MRSA strains (CCRI-9208, CCRI-9770, CCRI-9681, CCRI-9860) which harbor the MREP types vi, viii, ix and x described in the present invention remained undetectable.

EXAMPLE 8:

Developement of real-time PCR assays on the Smart Cycler[®] for detection and identification of MRSA based on MREP types vi, viii, ix. Upon analysis of the new MREP types vi, viii and ix sequence data described in the present invention, one new primers specific to MREP type vi (SEQ ID NO.: 201), one primer specific to MREP type viii (SEQ ID NO.: 115), a primer specific to MREP type ix (SEQ ID NO.: 109) and a primer specific to both MREP types viii and ix (SEQ ID NO.: 116) were designed. Each PCR primer was used in combination with the *orfX*-specific primer (SEQ ID NO.: 64) and tested against its specific target strain. Each PCR reaction contained 50 mM KCl, 10 mM Tris-HCl (pH 9.0), 0.1% Triton X-100, 3.45 mM MgCl₂, 0.4 µM of each of the SCC*mec*- and *orfX*-specific primers, 200 µM of each of the four dNTPs, 3.4 µg/µl of BSA, and 0.875

U *Taq* polymerase coupled with *TaqStart*TM Antibody. The PCR amplification was performed as described in Example 7. Sensitivity tests performed by using genomic DNA purified from their respective MRSA target strains showed that the best primer pair combination was SEQ ID NOs.: 64 and 115 for the detection of MREP types viii and ix simultaneously. These new *SCCmec*-specific primers may be used in multiplex with primers specific to MREP types i, ii, iii, iv, v and vii (SEQ ID NOs.: 64, 66, 67, 79 and 80) described in previous examples to provide a more ubiquitous MRSA assay.

In conclusion, we have improved the ubiquity of detection of MRSA strains. New MREJ types iv to x have been identified. Amongst strains representative of these new types, Hiramitsu's primers and/or probes succeeded in detecting less than 50% thereof. We have therefore amply passed the bar of at least 50% ubiquity, since our primers and probes were designed to detect 100% of the strains tested as representatives of MREJ types iv to ix. Therefore, although ubiquity depends on the pool of strains and representatives that are underanalyse, we know now that close to 100% ubiquity is an attainable goal, when using the sequences of the right junctions (MREJ) to derive probes and primers dealing with polymorphism in this region. Depending on how many unknown types of MREJ exist, we have a margin of manoeuvre going from 50% (higher than Hiramitsu's primers for the tested strains) to 100% if we sequence all the existing MREJs to derive properly the present diagnostic tools and methods, following the above teachings.

This invention has been described herein above, and it is readily apparent that modifications can be made thereto without departing from the spirit of this invention. These modifications are under the scope of this invention, as defined in the appended claims.

**Table 1. PCR amplification primers reported by Hiramatsu et al.
in US patent 6,156,507 found in the sequence listing**

| 5 | SEQ ID NO.: | Target | Position ^{a,b} | SEQ ID NO.: |
|----|---------------------|------------------------|-------------------------|---------------------|
| | (present invention) | | | (US pat. 6,156,507) |
| 10 | 52 | MREP types i and ii | 480 | 18 |
| | 53 | MREP types i and ii | 758 | 19 |
| | 54 | MREP types i and ii | 927 | 20 |
| | 55 | MREP types i and ii | 1154 | 21 |
| | 56 | MREP types i and ii | 1755 | 22 |
| | 57 | MREP types i and ii | 2302 | 23 |
| | 58 | MREP type iii | 295 ^c | 24 |
| | 59 | orfX | 1664 | 25 |
| 15 | 60 | orfSA0022 ^d | 3267 | 28 |
| | 61 | orfSA0022 ^d | 3585 | 27 |
| | 62 | orfX | 1389 | 26 |
| | 63 | orfSA0022 ^d | 2957 | 29 |

20

^a Position refers to nucleotide position of the 5' end of primer.

^b Numbering for SEQ ID NOs.: 52-57 refers to SEQ ID NO.: 2; numbering for SEQ ID NO.: 58 refers to SEQ ID NO.: 4; numbering for SEQ ID NOs.: 59-63 refers to SEQ ID NO.: 3.

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^c Primer is reverse-complement of target sequence.

^d orfSA0022 refers to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

5 Table 2. Specificity and ubiquity tests performed on a standard thermocycler using the optimal set of primers described by Hiramatsu et al. (SEQ ID NOs. : 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) for the detection of MRSA

| Strains | PCR results for SCCmec - <i>orfX</i> right extremity junction | |
|---------------------|---------------------------------------------------------------|--------------|
| | Positive (%) | Negative (%) |
| MRSA - 39 strains | 19 (48.7) | 20 (51.2) |
| MSSA - 41 strains | 13 (31.7) | 28 (68.3) |
| MRCNS - 9 strains* | 0 (0%) | 9 (100%) |
| MSCNS - 11 strains* | 0 (0%) | 11 (100%) |

10 * Details regarding CNS strains:

| | | |
|----|---------|-------------------------------|
| 15 | MRCNS : | <i>S. caprae</i> (1) |
| | | <i>S. cohnii cohnii</i> (1) |
| | | <i>S. epidermidis</i> (1) |
| | | <i>S. haemolyticus</i> (2) |
| | | <i>S. hominis</i> (1) |
| | | <i>S. sciuri</i> (1) |
| | | <i>S. simulans</i> (1) |
| | | <i>S. warneri</i> (1) |
| 25 | MSCNS : | <i>S. cohnii cohnii</i> (1) |
| | | <i>S. epidermidis</i> (1) |
| | | <i>S. equorum</i> (1) |
| | | <i>S. gallinarum</i> (1) |
| | | <i>S. haemolyticus</i> (1) |
| | | <i>S. lentus</i> (1) |
| | | <i>S. lugdunensis</i> (1) |
| | | <i>S. saccharolyticus</i> (1) |
| 30 | | <i>S. saprophyticus</i> (2) |
| | | <i>S. xylosus</i> (1) |

Table 3. Origin of MRSA strains not amplifiable using primers developed by Hiramatsu et al. (SEQ ID NOs.: 22, 24 and 28 in US patent 6,156,507 corresponding to SEQ ID NOs.: 56, 58 and 60, respectively, in the present invention) as well as primers developed in the present invention targeting MREP types i, ii and iii (SEQ ID NOs.: 64, 66 and 67)

| Staphylococcus aureus strain designation: | | Origin |
|----------------------------------------------|-------------------|-----------------|
| Original | CCRI ^a | |
| ATCC BAA-40 ^b | CCRI-9504 | Portugal |
| ATCC 33592 | CCRI-178 | USA |
| R991282 | CCRI-2025 | Québec, Canada |
| 4508 | CCRI-9208 | Québec, Canada |
| 19121 | CCRI-8895 | Denmark |
| Z109 | CCRI-8903 | Denmark |
| 45302 | CCRI-1263 | Ontario, Canada |
| R655 | CCRI-1324 | Québec, Canada |
| MA 50428 | CCRI-1311 | Québec, Canada |
| MA 50609 | CCRI-1312 | Québec, Canada |
| MA 51363 | CCRI-1331 | Québec, Canada |
| MA 51561 | CCRI-1325 | Québec, Canada |
| 14A0116 | CCRI-9681 | Poland |
| 23 (CCUG 41787) | CCRI-9860 | Sweden |
| SE26-1 | CCRI-9770 | Ontario, Canada |
| SE1-1 | CCRI-9583 | Ontario, Canada |
| ID-61880 ^c | CCRI-9589 | Ontario, Canada |
| SE47-1 | CCRI-9773 | Ontario, Canada |
| SE49-1 | CCRI-9774 | Ontario, Canada |
| 39795-2 | CCRI-1377 | Québec, Canada |

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

^b Portuguese clone.

^c Canadian clone EMRSA1.

Table 4. *Staphylococcus aureus* MREJ nucleotide sequences revealed in the present invention

| 5 | SEQ ID NO. | <i>Staphylococcus aureus</i> strain designation: | | Genetic Target |
|----|------------|--------------------------------------------------|-------------------|-------------------------------------------------------------------------|
| | | Original | CCRI ^a | |
| 10 | 27 | R991282 | CCRI-2025 | <i>mecA</i> |
| | 28 | 45302 | CCRI-1263 | <i>mecA</i> |
| | 29 | MA 50428 | CCRI-1311 | <i>mecA</i> |
| | 30 | MA 51363 | CCRI-1331 | <i>mecA</i> |
| | 31 | 39795-2 | CCRI-1377 | <i>mecA</i> and 1.5 kb of downstream region |
| 15 | 42 | ATCC 33592 | CCRI-178 | MREP type iv |
| | 43 | 19121 | CCRI-8895 | MREP type iv |
| | 44 | Z109 | CCRI-8903 | MREP type iv |
| | 45 | R655 | CCRI-1324 | MREP type iv |
| | 46 | MA 51363 | CCRI-1331 | MREP type iv |
| 20 | 47 | 45302 | CCRI-1263 | MREP type v |
| | 48 | 39795-2 | CCRI-1377 | MREP type v |
| | 49 | MA 50428 | CCRI-1311 | MREP type v |
| | 50 | R991282 | CCRI-2025 | MREP type v |
| | 51 | ATCC BAA-40 | CCRI-9504 | MREP type iv |
| 25 | 165 | SE1-1 | CCRI-9583 | MREP type vii |
| | 166 | ID-61880 | CCRI-9589 | MREP type vii |
| | 167 | 23 (CCUG 41787) | CCRI-9860 | MREP type viii |
| | 168 | 14A016 | CCRI-9681 | MREP type ix |
| | 171 | 4508 | CCRI-9208 | MREP type vi |
| 30 | 172 | SE26-1 | CCRI-9770 | <i>orfSA0021^b</i> and 75 bp of <i>orfSA0022^b</i> |
| | 173 | 26 (98/10618) | CCRI-9864 | MREP type ii |
| | 174 | 27 (98/26821) | CCRI-9865 | MREP type ii |
| | 175 | 28 (24344) | CCRI-9866 | MREP type ii |
| | 176 | 12 (62305) | CCRI-9867 | MREP type ii |
| 35 | 177 | 22 (90/14719) | CCRI-9868 | MREP type ii |
| | 178 | 23 (98/14719) | CCRI-9869 | MREP type ii |
| | 179 | 32 (97S99) | CCRI-9871 | MREP type ii |
| | 180 | 33 (97S100) | CCRI-9872 | MREP type ii |
| | 181 | 38 (825/96) | CCRI-9873 | MREP type ii |
| 40 | 182 | 39 (842/96) | CCRI-9874 | MREP type ii |
| | 183 | 43 (N8-892/99) | CCRI-9875 | MREP type ii |
| | 184 | 46 (9805-0137) | CCRI-9876 | MREP type iii |
| | 185 | 1 | CCRI-9882 | MREP type ii |
| | 186 | 29 | CCRI-9885 | MREP type ii |
| 45 | 189 | SE1-1 | CCRI-9583 | <i>mecA</i> and 2.2 kb of downstream region, including IS431 <i>mec</i> |
| | 190 | ATCC BAA-40 | CCRI-9504 | <i>mecA</i> and 1.5 kb of downstream region |
| | 191 | 4508 | CCRI-9208 | <i>mecA</i> and 0.9 kb of downstream region |
| | 192 | ID-61880 | CCRI-9589 | <i>mecA</i> and 0.9 kb of downstream region |
| | 193 | 14A016 | CCRI-9681 | <i>mecA</i> and 0.9 kb of downstream region |
| 50 | 195 | SE26-1 | CCRI-9770 | <i>mecA</i> and 1.5 kb of downstream region, including IS431 <i>mec</i> |
| | 197 | ATCC 43300 | CCRI-175 | MREP type ii |
| | 198 | R522 | CCRI-1262 | MREP type iii |
| | 199 | 13370 | CCRI-8894 | MREP type i |
| | 219 | ATCC BAA-40 | CCRI-9504 | <i>tetK</i> |

Table 4. *Staphylococcus aureus* MREJ nucleotide sequences revealed in the present invention (continued)

| 5 | SEQ ID NO. | <i>Staphylococcus aureus</i> strain designation: | | Genetic Target ^a |
|----|------------|--------------------------------------------------|-------------------|------------------------------------------------|
| | | Original | CCRI ^b | |
| 10 | 220 | MA 51363 | CCRI-1331 | <i>mecA</i> and 1.5 kb of downstream region |
| | 221 | 39795-2 | CCRI-1377 | IS431 <i>mec</i> and 0.6 kb of upstream region |
| | 222 | R991282 | CCRI-2025 | <i>mecA</i> and 1.5 kb of downstream region |
| | 223 | R991282 | CCRI-2025 | IS431 <i>mec</i> and 0.6 kb of upstream region |
| | 224 | 23 (CCUG 41787) | CCRI-9860 | <i>mecA</i> and 1.5 kb of downstream region |
| | 225 | 23 (CCUG 41787) | CCRI-9860 | IS431 <i>mec</i> and 0.6 kb of upstream region |
| | 233 | 14A016 | CCRI-9681 | MREP type ix |

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

^b *orfSA0021* and *orfSA0022* refer to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 5. PCR primers developed in the present invention

| | SEQ ID NO. | Target | Originating DNA | |
|----|------------|---------------------|-----------------------|------------|
| | | | Position ^a | SEQ ID NO. |
| 5 | 64 | <i>orfX</i> | 1720 | 3 |
| | 70 | <i>orfX</i> | 1796 | 3 |
| | 71 | <i>orfX</i> | 1712 | 3 |
| | 72 | <i>orfX</i> | 1749 | 3 |
| 10 | 73 | <i>orfX</i> | 1758 | 3 |
| | 74 | <i>orfX</i> | 1794 | 3 |
| | 75 | <i>orfX</i> | 1797 | 3 |
| | 76 | <i>orfX</i> | 1798 | 3 |
| 15 | 66 | MREP types i and ii | 2327 | 2 |
| | 100 | MREP types i and ii | 2323 | 2 |
| | 101 | MREP types i and ii | 2314 | 2 |
| | 97 | MREP type ii | 2434 | 2 |
| 20 | 99 | MREP type ii | 2434 | 2 |
| | 67 | MREP type iii | 207 ^b | 4 |
| | 98 | MREP type iii | 147 ^b | 4 |
| | 102 | MREP type iii | 251 ^b | 4 |
| 25 | 79 | MREP type iv | 74 ^b | 43 |
| | 80 | MREP type v | 50 ^b | 47 |
| | 109 | MREP type ix | 652 ^b | 168 |
| | 204 | MREP type vi | 642 ^b | 171 |
| 30 | 112 | MREP type vii | 503 ^b | 165 |
| | 113 | MREP type vii | 551 ^b | 165 |
| | 115 | MREP type viii | 514 ^b | 167 |
| | 116 | MREP type viii | 601 ^b | 167 |

^a Position refers to nucleotide position of 5' end of primer.

^b Primer is reverse-complement of target sequence.

Table 6. Molecular beacon probes developed in the present invention

| | SEQ ID NO. | Target | Position |
|----|------------|-------------|-------------------|
| 5 | 32 | <i>orfX</i> | 86 ^a |
| | 83 | <i>orfX</i> | 86 ^a |
| | 84 | <i>orfX</i> | 34 ^{a,b} |
| | 160 | <i>orfX</i> | 55 ^{a,b} |
| 10 | 161 | <i>orfX</i> | 34 ^{a,b} |
| | 162 | <i>orfX</i> | 114 ^a |
| | 163 | <i>orfX</i> | 34 ^{a,b} |
| | 164 | <i>orfX</i> | 34 ^{a,b} |

15

^a Position refers to nucleotide position of the 5' end of the molecular beacon's loop on SEQ ID NO.: 3.

^b Sequence of molecular beacon's loop is reverse-complement of SEQ ID NO.: 3.

Table 7. Length of amplicons obtained with the different primer pairs which are objects of the present invention

| | SEQ ID NO. | Target ^d | Amplicon length ^a |
|----|---------------------|--------------------------------------|------------------------------|
| 5 | 59/52 ^b | <i>orfX</i> /MREP type i and ii | 2079 (type i);2181 (type ii) |
| | 59/53 ^b | <i>orfX</i> /MREP type i and ii | 1801 (type i);1903 (type ii) |
| | 59/54 ^b | <i>orfX</i> /MREP type i and ii | 1632 (type i);1734 (type ii) |
| | 59/55 ^b | <i>orfX</i> /MREP type i and ii | 1405 (type i);1507 (type ii) |
| 10 | 59/56 ^b | <i>orfX</i> /MREP type i and ii | 804 (type i);906 (type ii) |
| | 59/57 ^b | <i>orfX</i> /MREP type i and ii | 257 (type i);359 (type ii) |
| | 60/52 ^b | <i>orfSA0022</i> /MREP type i and ii | 2794 (type i);2896 (type ii) |
| | 60/53 ^b | <i>orfSA0022</i> /MREP type i and ii | 2516 (type i);2618 (type ii) |
| | 60/54 ^b | <i>orfSA0022</i> /MREP type i and ii | 2347 (type i);2449 (type ii) |
| 15 | 60/55 ^b | <i>orfSA0022</i> /MREP type i and ii | 2120 (type i);2222 (type ii) |
| | 60/56 ^b | <i>orfSA0022</i> /MREP type i and ii | 1519 (type i);1621 (type ii) |
| | 60/57 ^b | <i>orfSA0022</i> /MREP type i and ii | 972 (type i);1074 (type ii) |
| | 61/52 ^b | <i>orfSA0022</i> /MREP type i and ii | 2476 (type i);2578 (type ii) |
| | 61/53 ^b | <i>orfSA0022</i> /MREP type i and ii | 2198 (type i);2300 (type ii) |
| 20 | 61/54 ^b | <i>orfSA0022</i> /MREP type i and ii | 2029 (type i);2131 (type ii) |
| | 61/55 ^b | <i>orfSA0022</i> /MREP type i and ii | 1802 (type i);1904 (type ii) |
| | 61/56 ^b | <i>orfSA0022</i> /MREP type i and ii | 1201 (type i);1303 (type ii) |
| | 61/57 ^b | <i>orfSA0022</i> /MREP type i and ii | 654 (type i);756 (type ii) |
| | 62/52 ^b | <i>orfX</i> /MREP type i and ii | 2354 (type i);2456 (type ii) |
| 25 | 62/53 ^b | <i>orfX</i> /MREP type i and ii | 2076 (type i);2178 (type ii) |
| | 62/54 ^b | <i>orfX</i> /MREP type i and ii | 1907 (type i);2009 (type ii) |
| | 62/55 ^b | <i>orfX</i> /MREP type i and ii | 1680 (type i);1782 (type ii) |
| | 62/56 ^b | <i>orfX</i> /MREP type i and ii | 1079 (type i);1181 (type ii) |
| | 62/57 ^b | <i>orfX</i> /MREP type i and ii | 532 (type i);634 (type ii) |
| 30 | 63/52 ^b | <i>orfSA0022</i> /MREP type i and ii | 3104 (type i);3206 (type ii) |
| | 63/53 ^b | <i>orfSA0022</i> /MREP type i and ii | 2826 (type i);2928 (type ii) |
| | 63/54 ^b | <i>orfSA0022</i> /MREP type i and ii | 2657 (type i);2759 (type ii) |
| | 63/55 ^b | <i>orfSA0022</i> /MREP type i and ii | 2430 (type i);2532 (type ii) |
| | 63/56 ^b | <i>orfSA0022</i> /MREP type i and ii | 1829 (type i);1931 (type ii) |
| 35 | 63/57 ^b | <i>orfSA0022</i> /MREP type i and ii | 1282 (type i);1384 (type ii) |
| | 59/58 ^b | <i>orfX</i> /MREP type iii | 361 |
| | 60/58 ^b | <i>orfSA0022</i> /MREP type iii | 1076 |
| | 61/58 ^b | <i>orfSA0022</i> /MREP type iii | 758 |
| | 62/58 ^b | <i>orfX</i> /MREP type iii | 656 |
| 40 | 63/58 ^b | <i>orfSA0022</i> /MREP type iii | 1386 |
| | 70/66 | <i>orfX</i> /MREP type i and ii | 100 (type i);202 (type ii) |
| | 70/67 | <i>orfX</i> /MREP type iii | 147 (type iii) |
| | 64/66 ^c | <i>orfX</i> /MREP type i and ii | 176 (type i);278 (type ii) |
| | 64/67 ^c | <i>orfX</i> /MREP type iii | 223 |
| 45 | 64/79 ^c | <i>orfX</i> /MREP type iv | 215 |
| | 64/80 ^c | <i>orfX</i> /MREP type v | 196 |
| | 64/97 ^c | <i>orfX</i> /MREP type ii | 171 |
| | 64/98 ^c | <i>orfX</i> /MREP type iii | 163 |
| | 64/99 ^c | <i>orfX</i> /MREP type ii | 171 |
| 50 | 64/100 ^c | <i>orfX</i> /MREP types i and ii | 180 (type i);282 (type ii) |
| | 64/101 ^c | <i>orfX</i> /MREP types i and ii | 189 (type i);291 (type ii) |
| | 64/102 ^c | <i>orfX</i> /MREP type iii | 263 |
| | 64/109 ^c | <i>orfX</i> /MREP type ix | 369 |
| | 64/204 ^c | <i>orfX</i> /MREP type vi | 348 |
| 55 | 64/112 ^c | <i>orfX</i> /MREP type vii | 214 |
| | 64/113 ^c | <i>orfX</i> /MREP type vii | 263 |
| | 64/115 ^c | <i>orfX</i> /MREP type viii | 227 |
| | 64/116 ^c | <i>orfX</i> /MREP type viii | 318 |

^a Amplicon length is given in base pairs for MREP types amplified by the set of primers.

^b Set of primers described by Hiramatsu et al. in US patent 6,156,507.

^c Set of primers developed in the present invention.

65 ^d *orfSA0022* refers to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 8. Other primers developed in the present invention

| | SEQ ID NO. | Target | Originating DNA | |
|----|------------|--------------------------------|-----------------------|------------|
| | | | Position ^a | SEQ ID NO. |
| 5 | 77 | MREP type iv | 993 | 43 |
| | 65 | MREP type v | 636 | 47 |
| | 70 | <i>orfX</i> | 1796 | 3 |
| | 68 | <i>IS431</i> | 626 | 92 |
| 10 | 69 | <i>mecA</i> | 1059 | 78 |
| | 96 | <i>mecA</i> | 1949 | 78 |
| | 81 | <i>mecA</i> | 1206 | 78 |
| | 114 | MREP type vii | 629 ^b | 165 |
| | 117 | MREP type ii | 856 | 194 |
| 15 | 118 | MREP type ii | 974 ^b | 194 |
| | 119 | MREP type vii | 404 | 189 |
| | 120 | MREP type vii | 477 ^b | 189 |
| | 123 | MREP type vii | 551 | 165 |
| | 124 | MREP type ii | 584 | 170 |
| 20 | 125 | MREP type ii | 689 ^b | 170 |
| | 126 | <i>orfSA0021</i> | 336 | 231 |
| | 127 | <i>orfSA0021</i> | 563 | 231 |
| | 128 | <i>orfSA0022^d</i> | 2993 | 231 |
| | 129 | <i>orfSA0022^d</i> | 3467 ^b | 231 |
| 25 | 132 | <i>orfX</i> | 3700 | 231 |
| | 145 | MREP type iv | 988 | 51 |
| | 146 | MREP type v | 1386 | 51 |
| | 147 | MREP type iv | 891 ^b | 51 |
| | 148 | MREP type ix | 664 | 168 |
| 30 | 149 | MREP type ix | 849 ^b | 168 |
| | 150 | MREP type vii | 1117 ^b | 165 |
| | 151 | MREP type vii | 1473 | 189 |
| | 152 | <i>IS431mec</i> | 1592 ^b | 189 |
| | 154 | MREP type v | 996 ^b | 50 |
| 35 | 155 | MREP type v | 935 | 50 |
| | 156 | <i>tetK</i> from plasmid pT181 | 1169 ^b | 228 |
| | 157 | <i>tetK</i> from plasmid pT181 | 136 | 228 |
| | 158 | <i>orfX</i> | 2714 ^b | 2 |
| | 159 | <i>orfX</i> | 2539 | 2 |
| 40 | 187 | MREP type viii | 967 ^b | 167 |
| | 188 | MREP type viii | 851 | 167 |

^a Position refers to nucleotide position of the 5' end of primer.

45 ^b Primer is reverse-complement of target sequence.

Table 9. Amplification and/or sequencing primers developed in the present invention

| 5 | SEQ ID NO. | Target | Originating DNA | |
|----|------------|-------------------------------------------------------------------|-----------------------|------------|
| | | | Position ^a | SEQ ID NO. |
| 10 | 85 | <i>S. aureus</i> chromosome | 197 ^b | 35 |
| | 86 | <i>S. aureus</i> chromosome | 198 ^b | 37 |
| | 87 | <i>S. aureus</i> chromosome | 197 ^b | 38 |
| | 88 | <i>S. aureus</i> chromosome | 1265 ^b | 39 |
| | 89 | <i>S. aureus</i> chromosome | 1892 | 3 |
| 15 | 103 | <i>orfX</i> | 1386 | 3 |
| | 105 | MREP type i | 2335 | 2 |
| | 106 | MREP type ii | 2437 | 2 |
| | 107 | MREP type iii | 153 ^b | 4 |
| | 108 | MREP type iii | 153 ^b | 4 |
| 20 | 121 | MREP type vii | 1150 | 165 |
| | 122 | MREP type vii | 1241 ^b | 165 |
| | 130 | <i>orfX</i> | 4029 ^b | 231 |
| | 131 | region between <i>orfSA0022</i> and <i>orfSA0023</i> ^d | 3588 | 231 |
| | 133 | <i>merB</i> from plasmid pI258 | 262 | 226 |
| 25 | 134 | <i>merB</i> from plasmid pI258 | 539 ^b | 226 |
| | 135 | <i>merR</i> from plasmid pI258 | 564 | 226 |
| | 136 | <i>merR</i> from plasmid pI258 | 444 | 227 |
| | 137 | <i>merR</i> from plasmid pI258 | 529 | 227 |
| | 138 | <i>merR</i> from plasmid pI258 | 530 ^b | 227 |
| 30 | 139 | <i>rep</i> from plasmid pUB110 | 796 | 230 |
| | 140 | <i>rep</i> from plasmid pUB110 | 761 ^b | 230 |
| | 141 | <i>rep</i> from plasmid pUB110 | 600 | 230 |
| | 142 | <i>aadD</i> from plasmid pUB110 | 1320 ^b | 229 |
| | 143 | <i>aadD</i> from plasmid pUB110 | 759 | 229 |
| 35 | 144 | <i>aadD</i> from plasmid pUB110 | 646 | 229 |
| | 153 | MREP type vii | 1030 | 165 |
| | 200 | <i>orfSA0022</i> ^d | 871 ^c | 231 |
| | 201 | <i>orfSA0022</i> ^d | 1006 | 231 |
| | 202 | MREP type vi | 648 | 171 |
| 40 | 203 | MREP type vi | 883 ^b | 171 |
| | 205 | MREP type ix | 1180 | 168 |
| | 206 | MREP type ix | 1311 ^b | 233 |
| | 207 | MREP type viii | 1337 | 167 |
| | 208 | MREP type viii | 1441 ^b | 167 |
| 45 | 209 | <i>ccrA</i> | 184 | 232 |
| | 210 | <i>ccrA</i> | 385 | 232 |
| | 211 | <i>ccrA</i> | 643 ^b | 232 |
| | 212 | <i>ccrA</i> | 1282 ^b | 232 |
| | 213 | <i>ccrB</i> | 1388 | 232 |
| 50 | 214 | <i>ccrB</i> | 1601 | 232 |
| | 215 | <i>ccrB</i> | 2139 ^b | 232 |
| | 216 | <i>ccrB</i> | 2199 ^b | 232 |
| | 217 | <i>ccrB</i> | 2847 ^b | 232 |
| | 218 | <i>ccrB</i> | 2946 ^b | 232 |

^a Position refers to nucleotide position of the 5' end of primer.

^b Primer is reverse-complement of target sequence.

55 ^c Primer contains two mismatches.

^d *orfSA0022* and *orfSA0023* refer to the open reading frame designation from GenBank accession number AP003129 (SEQ ID NO.: 231).

Table 10. Origin of the nucleic acids and/or sequences available from public databases found in the sequence listing

| | SEQ ID NO. | Staphylococcal strain | Source | Accession number | Genetic Target ^{a, b} |
|----|------------|-----------------------|-----------------------------|------------------|-----------------------------------------------------------|
| 5 | | | | | |
| | 1 | NCTC 10442 | Database | AB033763 | SCCmec type I MREJ |
| | 2 | N315 | Database | D86934 | SCCmec type II MREJ |
| 10 | 3 | NCTC 8325 | Database | AB014440 | MSSA chromosome |
| | 4 | 86/560 | Database | AB013471 | SCCmec type III MREJ |
| | 5 | 86/961 | Database | AB013472 | SCCmec type III MREJ |
| | 6 | 85/3907 | Database | AB013473 | SCCmec type III MREJ |
| | 7 | 86/2652 | Database | AB013474 | SCCmec type III MREJ |
| 15 | 8 | 86/1340 | Database | AB013475 | SCCmec type III MREJ |
| | 9 | 86/1762 | Database | AB013476 | SCCmec type III MREJ |
| | 10 | 86/2082 | Database | AB013477 | SCCmec type III MREJ |
| | 11 | 85/2111 | Database | AB013478 | SCCmec type III MREJ |
| | 12 | 85/5495 | Database | AB013479 | SCCmec type III MREJ |
| 20 | 13 | 85/1836 | Database | AB013480 | SCCmec type III MREJ |
| | 14 | 85/2147 | Database | AB013481 | SCCmec type III MREJ |
| | 15 | 85/3619 | Database | AB013482 | SCCmec type III MREJ |
| | 16 | 85/3566 | Database | AB013483 | SCCmec type III MREJ |
| | 17 | 85/2232 | Database | AB014402 | SCCmec type II MREJ |
| 25 | 18 | 85/2235 | Database | AB014403 | SCCmec type II MREJ |
| | 19 | MR108 | Database | AB014404 | SCCmec type II MREJ |
| | 20 | 85/9302 | Database | AB014430 | SCCmec type I MREJ |
| | 21 | 85/9580 | Database | AB014431 | SCCmec type I MREJ |
| | 22 | 85/1940 | Database | AB014432 | SCCmec type I MREJ |
| 30 | 23 | 85/6219 | Database | AB014433 | SCCmec type I MREJ |
| | 24 | 64/4176 | Database | AB014434 | SCCmec type I MREJ |
| | 25 | 64/3846 | Database | AB014435 | SCCmec type I MREJ |
| | 26 | HUC19 | Database | AF181950 | SCCmec type II MREJ |
| | 33 | G3 | US 6,156,507 | SEQ ID NO.: 15 | <i>S. epidermidis</i> |
| 35 | | | | | SCCmec type II MREJ |
| | 34 | SH 518 | US 6,156,507 | SEQ ID NO.: 16 | <i>S. haemolyticus</i> |
| | | | | | SCCmec type II MREJ |
| | 35 | ATCC 25923 | US 6,156,507 | SEQ ID NO.: 9 | <i>S. aureus</i> chromosome |
| | 36 | STP23 | US 6,156,507 | SEQ ID NO.: 10 | <i>S. aureus</i> chromosome |
| 40 | 37 | STP43 | US 6,156,507 | SEQ ID NO.: 12 | <i>S. aureus</i> chromosome |
| | 38 | STP53 | US 6,156,507 | SEQ ID NO.: 13 | <i>S. aureus</i> chromosome |
| | 39 | 476 | Genome project ^c | | <i>S. aureus</i> chromosome |
| | 40 | 252 | Genome project ^c | | SCCmec type II MREJ |
| | 41 | COL | Genome project ^d | | SCCmec type I MREJ |
| 45 | 78 | NCTC 8325 | Database | X52593 | <i>mecA</i> |
| | 82 | NCTC 10442 | Database | AB033763 | <i>mecA</i> |
| | 90 | N315 | Database | D86934 | <i>mecA</i> |
| | 91 | 85/2082 | Database | AB037671 | <i>mecA</i> |
| | 92 | NCTC 10442 | Database | AB033763 | IS431 |
| 50 | 93 | N315 | Database | D86934 | IS431 |
| | 94 | HUC19 | Database | AF181950 | IS431 |
| | 95 | NCTC 8325 | Database | X53818 | IS431 |
| | 104 | 85/2082 | Database | AB037671 | SCCmec type III MREJ |
| | 226 | unknown | Database | L29436 | <i>merB</i> on plasmid pI258 |
| 55 | 227 | unknown | Database | L29436 | <i>merR</i> on plasmid pI258 |
| | 228 | unknown | Database | S67449 | <i>tetK</i> on plasmid pT181 |
| | 229 | HUC19 | Database | AF181950 | <i>aadD</i> on plasmid pUB110 |
| | 230 | HUC19 | Database | AF181950 | <i>rep</i> on plasmid pUB110 |
| | 231 | N315 | Database | AP003129 | <i>orfSA0021</i> , <i>orfSA0022</i> , <i>orfSA0023</i> |
| 60 | 232 | 85/2082 | Database | AB037671 | <i>ccrA/ccrB</i> |

^a MREJ refers to *mec* right extremity junction and includes sequences from SCCmec-right extremity and chromosomal DNA to the right of SCCmec integration site.

^b Unless otherwise specified, all sequences were obtained from *S. aureus* strains.

65 ^c Sanger Institute genome project (<http://www.sanger.ac.uk>).

^d TIGR genome project (<http://www.tigr.org>).

Table 11. Analytical sensitivity of the MRSA-specific PCR assay targeting MREP types i, ii and iii on a standard thermocycler using the set of primers developed in the present invention (SEQ ID NOs.: 64, 66 and 67)

5

| Strain designation : | | Detection limit (number of genome copies) |
|----------------------|-------------------------------|----------------------------------------------|
| Original | CCRI ^a (MREP type) | |
| 13370 | CCRI-8894 (I) | 5 |
| ATCC 43300 | CCRI-175 (II) | 2 |
| 35290 | CCRI-1262 (III) | 2 |

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

Table 12. Specificity and ubiquity tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii and iii developed in the present invention (SEQ ID NOS.: 64, 66 and 67) for the detection of MRSA

5

| Strains | PCR results for MREJ | |
|---------------------|----------------------|--------------|
| | Positive (%) | Negative (%) |
| MRSA - 208 strains | 188 (90.4) | 20 (9.6) |
| MSSA - 252 strains | 13 (5.2) | 239 (94.8) |
| MRCNS - 41 strains* | 0 | 42 (100) |
| MSCNS - 21 strains* | 0 | 21 (100) |

* Details regarding CNS strains:

| | | |
|----|---------|----------------------------------|
| 10 | MRCNS : | <i>S. caprae</i> (2) |
| | | <i>S. cohnii cohnii</i> (3) |
| | | <i>S. cohnii urealyticum</i> (4) |
| | | <i>S. epidermidis</i> (8) |
| | | <i>S. haemolyticus</i> (9) |
| | | <i>S. hominis</i> (4) |
| 15 | | <i>S. sciuri</i> (4) |
| | | <i>S. sciuri sciuri</i> (1) |
| | | <i>S. simulans</i> (3) |
| | | <i>S. warneri</i> (3) |
| 20 | MSCNS : | <i>S. cohnii cohnii</i> (1) |
| | | <i>S. epidermidis</i> (3) |
| | | <i>S. equorum</i> (2) |
| | | <i>S. felis</i> (1) |
| | | <i>S. gallinarum</i> (1) |
| | | <i>S. haemolyticus</i> (1) |
| 25 | | <i>S. hominis</i> (1) |
| | | <i>S. lentus</i> (1) |
| | | <i>S. lugdunensis</i> (1) |
| | | <i>S. saccharolyticus</i> (1) |
| 30 | | <i>S. saprophyticus</i> (5) |
| | | <i>S. simulans</i> (1) |
| | | <i>S. warneri</i> (1) |
| | | <i>S. xylosus</i> (1) |

Table 13. Percentage of sequence identity for the first 500 nucleotides of SCCmec right extremities between all 9 types of MREP^{a,b}

| MREP type | i | ii | iii | iv | v | vi | vii | viii | ix |
|-----------|----|------|------|------|------|------|------|------|------|
| i | -- | 79.2 | 42.8 | 42.8 | 41.2 | 44.4 | 44.6 | 42.3 | 42.1 |
| ii | | | 43.9 | 47.5 | 44.7 | 41.7 | 45.0 | 52.0 | 57.1 |
| iii | | | | 46.8 | 44.5 | 42.9 | 45.0 | 42.8 | 45.2 |
| iv | | | | | 45.8 | 41.4 | 44.3 | 48.0 | 41.3 |
| v | | | | | | 45.4 | 43.7 | 47.5 | 44.3 |
| vi | | | | | | | 45.1 | 41.1 | 47.2 |
| vii | | | | | | | | 42.8 | 40.9 |
| viii | | | | | | | | | 55.2 |
| ix | | | | | | | | | -- |

5

^a "First 500 nucleotides" refers to the 500 nucleotides within the SCCmec right extremity, starting from the integration site of SCCmec in the *Staphylococcus aureus* chromosome as shown on Figure 4.

10 ^b Sequences were extracted from SEQ ID NOs.: 1, 2, 104, 51, 50, 171, 165, 167, and 168 for types i to ix, respectively.

Table 14. Reference strains used to test sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences

| Staphylococcal species | Strains | Source ^a |
|------------------------|-------------------|---------------------|
| MRSA (n = 45) | 33591 | ATCC |
| | 33592 | ATCC |
| | 33593 | ATCC |
| | BAA-38 | ATCC |
| | BAA-39 | ATCC |
| | BAA-40 | ATCC |
| | BAA-41 | ATCC |
| | BAA-42 | ATCC |
| | BAA-43 | ATCC |
| | BAA-44 | ATCC |
| | F182 | CDC |
| | 23 (CCUG 41787) | HARMONY Collection |
| | ID-61880 (EMRSA1) | LSPQ |
| | MA 8628 | LSPQ |
| | MA 50558 | LSPQ |
| | MA 50428 | LSPQ |
| | MA 50609 | LSPQ |
| | MA 50884 | LSPQ |
| | MA 50892 | LSPQ |
| | MA 50934 | LSPQ |
| | MA 51015 | LSPQ |
| | MA 51056 | LSPQ |
| | MA 51085 | LSPQ |
| | MA 51172 | LSPQ |
| | MA 51222 | LSPQ |
| | MA 51363 | LSPQ |
| | MA 51561 | LSPQ |
| | MA 52034 | LSPQ |
| | MA 52306 | LSPQ |
| | MA 51520 | LSPQ |
| | MA 51363 | LSPQ |
| | 98/10618 | HARMONY Collection |
| | 98/26821 | HARMONY Collection |
| | 24344 | HARMONY Collection |
| | 62305 | HARMONY Collection |
| | 90/10685 | HARMONY Collection |
| | 98/14719 | HARMONY Collection |
| | 97S99 | HARMONY Collection |
| | 97S100 | HARMONY Collection |
| | 825/96 | HARMONY Collection |
| | 842/96 | HARMONY Collection |
| | N8-890/99 | HARMONY Collection |
| | 9805-01937 | HARMONY Collection |
| | 1 | Kreiswirth-1 |
| | 29 | Kreiswirth-1 |
| MRCNS (n = 4) | 29060 | ATCC |
| | 35983 | ATCC |
| | 35984 | ATCC |
| | 2514 | LSPQ |

Table 14. Reference strains used to test sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences(continued)

| Staphylococcal species | Strains | Source |
|------------------------|------------|------------------|
| MSSA (n = 28) | MA 52263 | LSPQ |
| | 6538 | ATCC |
| | 13301 | ATCC |
| | 25923 | ATCC |
| | 27660 | ATCC |
| | 29213 | ATCC |
| | 29247 | ATCC |
| | 29737 | ATCC |
| | RN 11 | CDC |
| | RN 3944 | CDC |
| | RN 2442 | CDC |
| | 7605060113 | CDC |
| | BM 4611 | Institut Pasteur |
| | BM 3093 | Institut Pasteur |
| | 3511 | LSPQ |
| | MA 5091 | LSPQ |
| | MA 8849 | LSPQ |
| | MA 8871 | LSPQ |
| | MA 50607 | LSPQ |
| | MA 50612 | LSPQ |
| | MA 50848 | LSPQ |
| | MA 51237 | LSPQ |
| | MA 51351 | LSPQ |
| | MA 52303 | LSPQ |
| | MA 51828 | LSPQ |
| | MA 51891 | LSPQ |
| | MA 51504 | LSPQ |
| | MA 52535 | LSPQ |
| | MA 52783 | LSPQ |
| MSCNS (n = 17) | 12228 | ATCC |
| | 14953 | ATCC |
| | 14990 | ATCC |
| | 15305 | ATCC |
| | 27836 | ATCC |
| | 27848 | ATCC |
| | 29070 | ATCC |
| | 29970 | ATCC |
| | 29974 | ATCC |
| | 35539 | ATCC |
| | 35552 | ATCC |
| | 35844 | ATCC |
| | 35982 | ATCC |
| | 43809 | ATCC |
| | 43867 | ATCC |
| | 43958 | ATCC |
| | 49168 | ATCC |

5

^a ATCC stands for "American Type Culture Collection".
LSPQ stands for "Laboratoire de Santé Publique du Québec".
CDC stands for "Center for Disease Control and Prevention".

Table 15. Clinical isolates used to test the sensitivity and/or specificity and/or ubiquity of the MRSA-specific PCR assays targeting MREJ sequences

| Staphylococcal species | Number of strains | Source |
|------------------------|-------------------|-----------|
| MRSA (n = 177) | 150 | Canada |
| | 10 | China |
| | 10 | Denmark |
| | 9 | Argentina |
| | 1 | Egypt |
| | 1 | Sweden |
| | 1 | Poland |
| | 3 | Japan |
| | 1 | France |
| MSSA (n = 224) | 208 | Canada |
| | 10 | China |
| | 4 | Japan |
| | 1 | USA |
| | 1 | Argentina |
| MRCNS (n = 38) | 32 | Canada |
| | 3 | China |
| | 1 | France |
| | 1 | Argentina |
| | 1 | USA |
| MSCNS (n = 17) | 14 | UK |
| | 3 | Canada |

5 **Table 16. Analytical sensitivity of tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NOs.: 64, 66, 67, 79 and 80) developed in the present invention for the detection and identification of MRSA**

| <i>Staphylococcus aureus</i> strain designation: | | Detection limit (number of genome copies) |
|-----------------------------------------------------|-------------------------------|----------------------------------------------|
| Original | CCRI ^a (MREP type) | |
| 13370 | CCRI-8894 (i) | 10 |
| ATCC 43300 | CCRI-175 (ii) | 5 |
| 9191 | CCRI-2086 (ii) | 10 |
| 35290 | CCRI-1262 (iii) | 5 |
| 352 | CCRI-1266 (iii) | 10 |
| 19121 | CCRI-8895 (iv) | 5 |
| ATCC 33592 | CCRI-178 (iv) | 5 |
| MA 50428 | CCRI-1311 (v) | 5 |
| R991282 | CCRI-2025 (v) | 5 |

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

5 **Table 17. Specificity and ubiquity tests performed on a standard thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NO.: 64, 66, 67, 79 and 80) developed in the present invention for the detection and identification of MRSA**

| Strains | PCR results for SCCmec - orfX right extremity junction | |
|--------------------------------|--------------------------------------------------------|--------------|
| | Positive (%) | Negative (%) |
| MRSA - 35 strains ^a | 27 (77.1) | 8 (22.9) |
| MSSA - 44 strains | 13 (29.5) | 31 (70.5) |
| MRCNS - 9 strains* | 0 | 9 (100) |
| MSCNS - 10 strains* | 0 | 10 (100) |

^a MRSA strains include the 20 strains listed in Table 3.

10

*Details regarding CNS strains:

| | | |
|----|---------|-------------------------------|
| 15 | MRCNS : | <i>S. caprae</i> (1) |
| | | <i>S. cohnii cohnii</i> (1) |
| | | <i>S. epidermidis</i> (1) |
| | | <i>S. haemolyticus</i> (2) |
| | | <i>S. hominis</i> (1) |
| | | <i>S. sciuri</i> (1) |
| | | <i>S. simulans</i> (1) |
| | | <i>S. warneri</i> (1) |
| 25 | MSCNS : | <i>S. cohnii</i> (1) |
| | | <i>S. epidermidis</i> (1) |
| | | <i>S. equorum</i> (1) |
| | | <i>S. haemolyticus</i> (1) |
| | | <i>S. lentus</i> (1) |
| | | <i>S. lugdunensis</i> (1) |
| | | <i>S. saccharolyticus</i> (1) |
| | | <i>S. saprophyticus</i> (2) |
| 30 | | <i>S. xylosus</i> (1) |

5

Table 18. Analytical sensitivity of tests performed on the Smart Cyclor[®] thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NOs.: 64, 66, 67, 79 and 80) and molecular beacon probe (SEQ ID NO.: 84) developed in the present invention for the detection and identification of MRSA

| <i>Staphylococcus aureus</i> strain designation: | | Detection limit (number of genome copies) |
|-----------------------------------------------------|-------------------------------|----------------------------------------------|
| Original | CCRI ^a (MREP type) | |
| 13370 | CCRI-8894 (i) | 2 |
| ATCC 43300 | CCRI-175 (ii) | 2 |
| 9191 | CCRI-2086 (ii) | 10 |
| 35290 | CCRI-1262 (iii) | 2 |
| 352 | CCRI-1266 (iii) | 10 |
| ATCC 33592 | CCRI-178 (iv) | 2 |
| MA 51363 | CCRI-1331 (iv) | 5 |
| 19121 | CCRI-8895 (iv) | 10 |
| Z109 | CCRI-8903 (iv) | 5 |
| 45302 | CCRI-1263 (v) | 10 |
| MA 50428 | CCRI-1311 (v) | 5 |
| MA 50609 | CCRI-1312 (v) | 5 |
| MA 51651 | CCRI-1325 (v) | 10 |
| 39795-2 | CCRI-1377 (v) | 10 |
| R991282 | CCRI-2025 (v) | 2 |

10

^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

5 Table 19. Specificity and ubiquity tests performed on the Smart Cyclor[®] thermocycler using the set of primers targeting MREP types i, ii, iii, iv and v (SEQ ID NO. : 64, 66, 67, 79 and 80) and molecular beacon probe (SEQ ID NO. : 84) developed in the present invention for the detection of MRSA

| Strains | PCR results for MREJ | |
|--------------------------------|----------------------|--------------|
| | Positive (%) | Negative (%) |
| MRSA - 29 strains ^a | 21 (72.4) | 8 (27.6) |
| MSSA - 35 strains | 13 (37.1) | 22 (62.9) |
| MRCNS - 14 strains | 0 | 14 (100) |
| MSCNS - 10 strains | 0 | 10 (100) |

10 ^a MRSA strains include the 20 strains listed in Table 3.

Details regarding CNS strains:

15 MRCNS : *S. epidermidis* (1)
S. haemolyticus (5)
S. simulans (5)
S. warneri (3)

20 MSCNS : *S. cohnii cohnii* (1)
S. epidermidis (1)
S. gallinarum (1)
S. haemolyticus (1)
S. lentus (1)
S. lugdunensis (1)
S. saccharolyticus (1)
25 *S. saprophyticus* (2)
S. xylosus (1).

5 Table 20. Analytical sensitivity of tests performed on the Smart
Cycler[®] thermocycler using the set of primers targeting
MREP types i, ii, iii, iv, v and vii (SEQ ID NOs.: 64,
66, 67, 79 and 80) and molecular beacon probe (SEQ ID
NO.: 84) developed in the present invention for the
detection and identification of MRSA

| Staphylococcus aureus strain designation: | | Detection limit |
|----------------------------------------------|-------------------------------|---------------------------|
| Original | CCRI ^a (MREP type) | (number of genome copies) |
| 13370 | CCRI-8894 (i) | 2 |
| ATCC 43300 | CCRI-175 (ii) | 2 |
| 35290 | CCRI-1262 (iii) | 2 |
| ATCC 33592 | CCRI-178 (iv) | 2 |
| R991282 | CCRI-2025 (v) | 2 |
| SE-41-1 | CCRI-9771 (vii) | 2 |

10 ^a CCRI stands for "Collection of the Centre de Recherche en Infectiologie".

5 Table 21. Specificity and ubiquity tests performed on the Smart
Cycler[®] thermocycler using the set of primers targeting
MREP types i, ii, iii, iv, vi and vii (SEQ ID NOs.: 64,
66, 67, 79 and 80) and molecular beacon probe (SEQ ID
NO.: 84) developed in the present invention for the
detection and identification of MRSA

| Strains | PCR results for MREJ | |
|--------------------------------|----------------------|--------------|
| | Positive (%) | Negative (%) |
| MRSA - 23 strains ^a | 19 (82.6) | 4 (17.4) |
| MSSA - 25 strains | 13 (52) | 12 (48) |
| MRCNS - 26 strains | 0 | 26 (100) |
| MSCNS - 8 strains | 0 | 8 (100) |

10 ^a MRSA strains include the 20 strains listed in Table 3.

Details regarding CNS strains:

15 MRCNS : *S. capitis* (2)
S. caprae (1)
S. cohnii (1)
S. epidermidis (9)
S. haemolyticus (5)
S. hominis (2)
20 *S. saprophyticus* (1)
S. sciuri (2)
S. simulans (1)
S. warneri (2)

25 MSCNS : *S. cohnii cohnii* (1)
S. epidermidis (1)
S. haemolyticus (1)
S. lugdunensis (1)
S. saccharolyticus (1)
30 *S. saprophyticus* (2)
S. xylosus (1)

Annex I: Strategy for the selection of specific amplification primers for types i and ii MREP

| Types i and ii MREP | | orFX | |
|---------------------|-----|----------------------------------|--------------------------------|
| SEQ ID NO.: | | 2358 | 2583 |
| 2324 | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 2 | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 1 | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 17 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 18 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 19 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 20 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 21 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 22 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 23 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 24 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 25 ^a | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 26 | TAT | GTCAAAAATC ATGAACCTCA TTACTTATGA | TA...CCT TGTGCAGGCC GTTTGATCCG |
| 33 ^c | | | CtT gGTGtAaaCC aTTgAgCCa |
| 34 ^c | | | CCT caTGCAtCC aTTTGATC |

Selected sequence for type i MREP and ii primer (SEQ ID No.: 66)

GTCAAAAATC ATGAACCTCA TTACTTATG

Selected sequence for orFX primer^b (SEQ ID NO.: 64)

TGTGCAGGCC GTTTGATCC

The sequence positions refer to SEQ ID NO.: 2.

Nucleotides in capitals are identical to the selected sequences or match those sequences. Mismatches are indicated by lower-case letters. Dots indicate gaps in the displayed sequences.

^a These sequences are the reverse-complements of SEQ ID NOs.: 17-25.
^b This sequence is the reverse-complement of the selected primer.
^c SEQ ID NOs.: 33 and 34 were obtained from CNS species.

Annex II: Strategy for the selection of a specific molecular beacon probe for the real-time detection of MREJ

| SEQ ID NO. : | 327 | orfx | 371 |
|-------------------|-------------|-----------------------|-------|
| 165 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 180 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 181 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 182 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 183 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 184 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 186 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 174 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 175 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 178 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 176 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 173 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 177 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 169 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 199 | ACAAG GACGT | CTTACAACGC AGTAACTATG | CACTA |
| 33 ^{a,b} | ACcAa GACGT | CTTACAACGC AGcAACTATG | CttTA |
| 34 ^{a,b} | AtgAG GACGT | CTTACAACGC AGcAACTATG | CACtT |

Selected sequence for orfx molecular beacon probes (SEQ ID NO.:163)^c (SEQ ID NO.:164)^c (SEQ ID NO.: 84)^c

GACGT CTTACAACGC AGTAACTATG
GACGT CTTACAACGC AGTAACTATG
GACGT CTTACAACGC AGTAACTATG

Nucleotide discrepancies between the orfx sequences and SEQ ID NO.: 84 are shown in lower-case. Other entries in the sequence listing also present similar variations. The stem of the molecular beacon probes are not shown for sake of clarity. The sequence positions refer to SEQ ID NO.:165.

^a These sequences are the reverse-complements of SEQ ID NOS.: 33 and 34.
^b SEQ ID NOS.: 33 and 34 were obtained from CNS species.
^c The sequences presented are the reverse-complement of the selected molecular beacon probes.

CLAIMS

What is claimed is :

- 5 1. A method to detect the presence of a methicillin-resistant *Staphylococcus aureus* (MRSA) strain in a sample, said MRSA strain being resistant because of the presence of an SCCmec insert containing a *mecA* gene, said SCCmec being inserted in bacterial nucleic acids thereby generating a polymorphic right extremity junction (MREJ), said method comprising the step of annealing the nucleic acids of the sample with a plurality of probes
10 and/or primers, characterized by:
- (i) said primers and/or probes are specific for MRSA strains and capable of annealing with polymorphic MREJ nucleic acids, said polymorphic MREJ comprising MREJ types i to x; and
15 (ii) said primers and/or probes altogether can anneal with at least four MREJ types selected from MREJ types i to x.
2. The method of claim 1, wherein the primers and/or probes are all chosen to anneal under common annealing conditions.
20
3. The method of claim 2, wherein the primer and/or probes are placed altogether in the same physical enclosure.
4. The method of any one of claims 1 to 3, wherein the primers and/or probes have at
25 least 10 nucleotides in length and are capable of annealing with MREJ types i to iii, defined in any one of SEQ ID NOs: 1, 20, 21, 22, 23, 24, 25, 41; 199 ; 2, 17, 18, 19, 26, 40, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 185, 186, 197 ; 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 104, 184, 198 ;
and with one or more of MREJ types iv to ix, having SEQ ID NOs: 42, 43, 44, 45, 46, 51 ;
30 47, 48, 49, 50 ; 171 ; 165, 166 ; 167 ; 168.
5. The method of any one of claims 1 to 4, wherein the primers and/or probes altogether can anneal with said SEQ ID NOs of MREJ types i to ix.

6. The method of any one of claims 1 to 5, wherein said primers and/or probes have the following sequences SEQ ID NOs:

- | | | |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------|
| 5 | 66, 100, 101, 105, 52, 53, 54, 55, 56, 57, 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159, 59, 62, 126, 127, 128, 129, 131, 200, 201, 60, 61, 63 | for the detection of MREJ type i |
| 10 | 32, 83, 84, 160, 161, 162, 163, 164 85, 86, 87, 88, 89 | |
| | 66, 97, 99, 100, 101, 106, 117, 118, 124, 125, 52, 53, 54, 55, 56, 57 | for the detection of MREJ type ii |
| 15 | 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159 59, 62 126, 127 128, 129, 131, 200, 201 | |
| 20 | 60, 61, 63 32, 83, 84, 160, 161, 162, 163, 164 85, 86, 87, 88, 89 | |
| | 67, 98, 102, 107, 108 | for the detection of MREJ type iii |
| 25 | 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159 58, 59, 62 126, 127 | |
| 30 | 128, 129, 131, 200, 201 60, 61, 63 32, 83, 84, 160, 161, 162, 163, 164 85, 86, 87, 88, 89 | |
| 35 | 79, 77, 145, 147 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159 59, 62 126, 127 | for the detection of MREJ type iv |
| 40 | 128, 129, 131, 200, 201 60, 61, 63 68 32, 83, 84, 160, 161, 162, 163, 164 85, 86, 87, 88, 89 | |
| 45 | | |
| | 65, 80, 146, 154, 155 64, 71, 72, 73, 74, 75, 76, 70, 103, 130, 132, 158, 159 59, 62 | for the detection of MREJ type v |
| 50 | 126, 127 | |

- 128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89
- 5
- 202, 203, 204 for the detection of MREJ type vi
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
59, 62
- 10 126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
85, 86, 87, 88, 89
- 15
- 112, 113, 114, 119, 120, 121, 122 for the detection of MREJ type vii
, 123, 150, 151, 153
64, 71, 72, 73, 74, 75, 76, 70, 103,
130, 132, 158, 159
- 20 59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
- 25 85, 86, 87, 88, 89
- 115, 116, 187, 188, 207, 208 for the detection of MREJ type viii
64, 71, 72, 73, 74, 75, 76, 70,
103, 130, 132, 158, 159
- 30 59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
- 35 85, 86, 87, 88, 89
- 109, 148, 149, 205, 206 for the detection of MREJ type ix.
64, 71, 72, 73, 74, 75, 76
70, 103, 130, 132, 158, 159
- 40 59, 62
126, 127
128, 129, 131, 200, 201
60, 61, 63
32, 83, 84, 160, 161, 162, 163, 164
- 45 85, 86, 87, 88, 89

7. The method of claim 6, wherein primer pairs have the nucleotide sequence which are defined in SEQ ID NOs :

50

- 64/66, 64/100, 64/101; 59/52,
59/53, 59/54, 59/55, 59/56, 59/57,
60/52, 60/53, 60/54, 60/55, 60/56
60/57, 61/52, 61/53, 61/54, 61/55
5 61/56, 61/57, 62/52, 62/53, 62/54
62/55, 62/56, 62/57, 63/52, 63/53
63/54, 63/55, 63/56, 63/57
- 64/66, 64/97, 64/99, 64/100, 64/101
10 59/52, 59/53, 59/54, 59/55, 59/56,
59/57, 60/52, 60/53, 60/54, 60/55,
60/56, 60/57, 61/52, 61/53, 61/54,
61/55, 61/56, 61/57, 62/52, 62/53,
62/54, 62/55, 62/56, 62/57, 63/52
15 63/53, 63/54, 63/55, 63/56, 63/57
- 64/67, 64/98, 64/102 ; 59/58,
60/58, 61/58, 62/58, 63/58
- 20 64/79
64/80
64/204
64/112, 64/113
64/115, 64/116
25 64/109
8. The method of claim 7, further comprising probes having the following sequences:
30 SEQ ID NOs: 32, 83, 84, 160, 161, 162, 163, 164 for the detection of MREJ types i to ix.
9. The method of any one of claims 6 to 8, wherein said primers and probes have the following nucleotide sequences:
- 35 vii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type i
viii) SEQ ID NOs: 64, 66, 84, 163, 164 for the detection of MREJ type ii
ix) SEQ ID NOs: 64, 67, 84, 163, 164 for the detection of MREJ type iii
x) SEQ ID NOs: 64, 79, 84, 163, 164 for the detection of MREJ type iv
xi) SEQ ID NOs: 64, 80, 84, 163, 164 for the detection of MREJ type v
xii) SEQ ID NOs: 64, 112, 84, 163, 164 for the detection of MREJ type vii.
- 40
10. The method of any one of claims 1 to 8, wherein said probes and primers are used together.

11. The method of claim 9 or 10, wherein said probes and/or primers are used together in the same physical enclosure.
12. A method for typing a MREJ of a MRSA strain, which comprises the steps of:
 5 reproducing the method of any one of claims 1 to 11 with primers and/or probes specific for a determined MREJ type, and detecting an annealed probe and/or primer as an indication of the presence of a determined MREJ type.
- 10 13. A nucleic acid selected from:
 vii) SEQ ID NOs: 42, 43, 44, 45, 46, 51 for sequence of MREJ type iv ;
 viii) SEQ ID NOs: 47, 48, 49, 50 for sequence of MREJ type v ;
 ix) SEQ ID NOs: 171 for sequence of MREJ type vi ;
 x) SEQ ID NOs: 165, 166 for sequence of MREJ type vii ;
 15 xi) SEQ ID NOs: 167 for sequence of MREJ type viii ;
 xii) SEQ ID NOs: 168 for sequence of MREJ type ix.
14. An oligonucleotide of at least 10 nucleotides in length which hybridizes with the nucleic acid of claim 13 and which hybridizes with one or more MREJ of types selected
 20 from iv to ix.
15. An oligonucleotide pair which has the nucleotide sequences defined in any one of SEQ ID NOs:
- | | | |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------|
| 25 | 64/66, 64/100, 64/101; 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56 60/57, 61/52, 61/53, 61/54, 61/55 61/56, 61/57, 62/52, 62/53, 62/54 30 62/55, 62/56, 62/57, 63/52, 63/53 63/54, 63/55, 63/56, 63/57 | for the detection of type i MREJ |
| 35 | 64/66, 64/97, 64/99, 64/100, 64/101 59/52, 59/53, 59/54, 59/55, 59/56, 59/57, 60/52, 60/53, 60/54, 60/55, 60/56, 60/57, 61/52, 61/53, 61/54, 61/55, 61/56, 61/57, 62/52, 62/53, 62/54, 62/55, 62/56, 62/57, 63/52 40 63/53, 63/54, 63/55, 63/56, 63/57 | for the detection of type ii MREJ |

64/67, 64/98, 64/102 ; 59/58,
60/58, 61/58, 62/58, 63/58

for the detection of type iii MREJ

64/79

for the detection of type iv MREJ

5 64/80

for the detection of type v MREJ

64/204

for the detection of type vi MREJ

64/112, 64/113

for the detection of type vii MREJ

64/115, 64/116

for the detection of type viii MREJ

64/109

for the detection of type ix MREJ

10

16. An oligonucleotide which has the nucleotide sequence defined in any one of SEQ ID
15 NOs: 32, 83, 84, 160, 161, 162, 163, 164.

17. A composition of matter comprising primers and/or probes, the nucleotide sequences
of which have at least 10 nucleotides in length which hybridize with any nucleic acid defined
in claim 13, and which hybridize with one or more MREJ of types selected from iv to ix.

20

18. The composition of claim 17, which further comprises primers and/or probes, which
hybridize with one or more MREJ of types selected from i to iii.

19. The composition of claim 18 or 19, wherein the primers pairs have the nucleotide
25 sequences defined in SEQ ID NOs:

30 64/66, 64/100, 64/101; 59/52,
59/53, 59/54, 59/55, 59/56, 59/57,
60/52, 60/53, 60/54, 60/55, 60/56
60/57, 61/52, 61/53, 61/54, 61/55
61/56, 61/57, 62/52, 62/53, 62/54
62/55, 62/56, 62/57, 63/52, 63/53
63/54, 63/55, 63/56, 63/57

for the detection of type i MREJ

35 64/66, 64/97, 64/99, 64/100, 64/101
59/52, 59/53, 59/54, 59/55, 59/56,
59/57, 60/52, 60/53, 60/54, 60/55,
60/56, 60/57, 61/52, 61/53, 61/54,
61/55, 61/56, 61/57, 62/52, 62/53,
40 62/54, 62/55, 62/56, 62/57, 63/52
63/53, 63/54, 63/55, 63/56, 63/57

for the detection of type ii MREJ

64/67, 64/98, 64/102 ; 59/58,
60/58, 61/58, 62/58, 63/58

for the detection of type iii MREJ

64/79

for the detection of type iv MREJ

5 64/80

for the detection of type v MREJ

64/204

for the detection of type vi MREJ

64/112, 64/113

for the detection of type vii MREJ

64/115, 64/116

for the detection of type viii MREJ

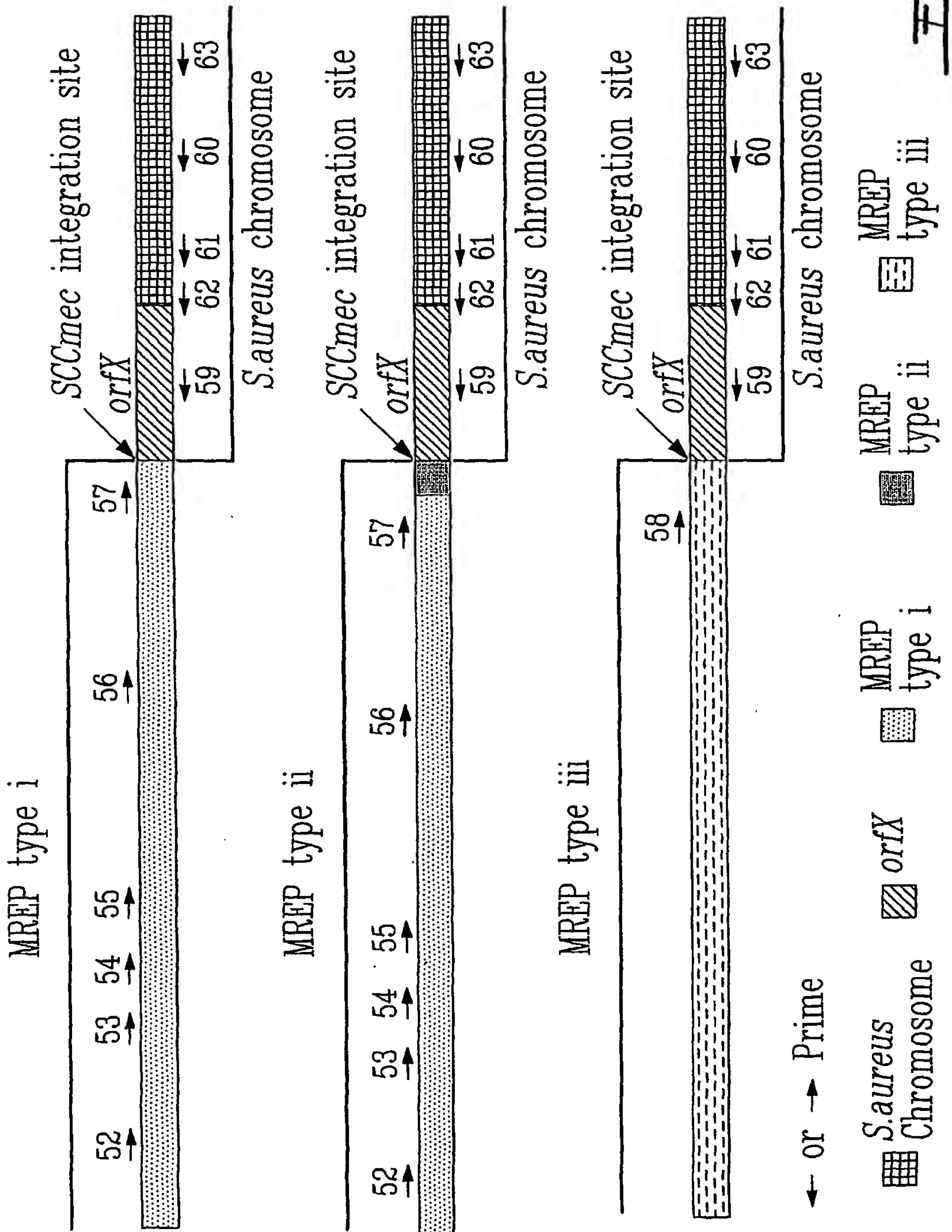
64/109

for the detection of type ix MREJ

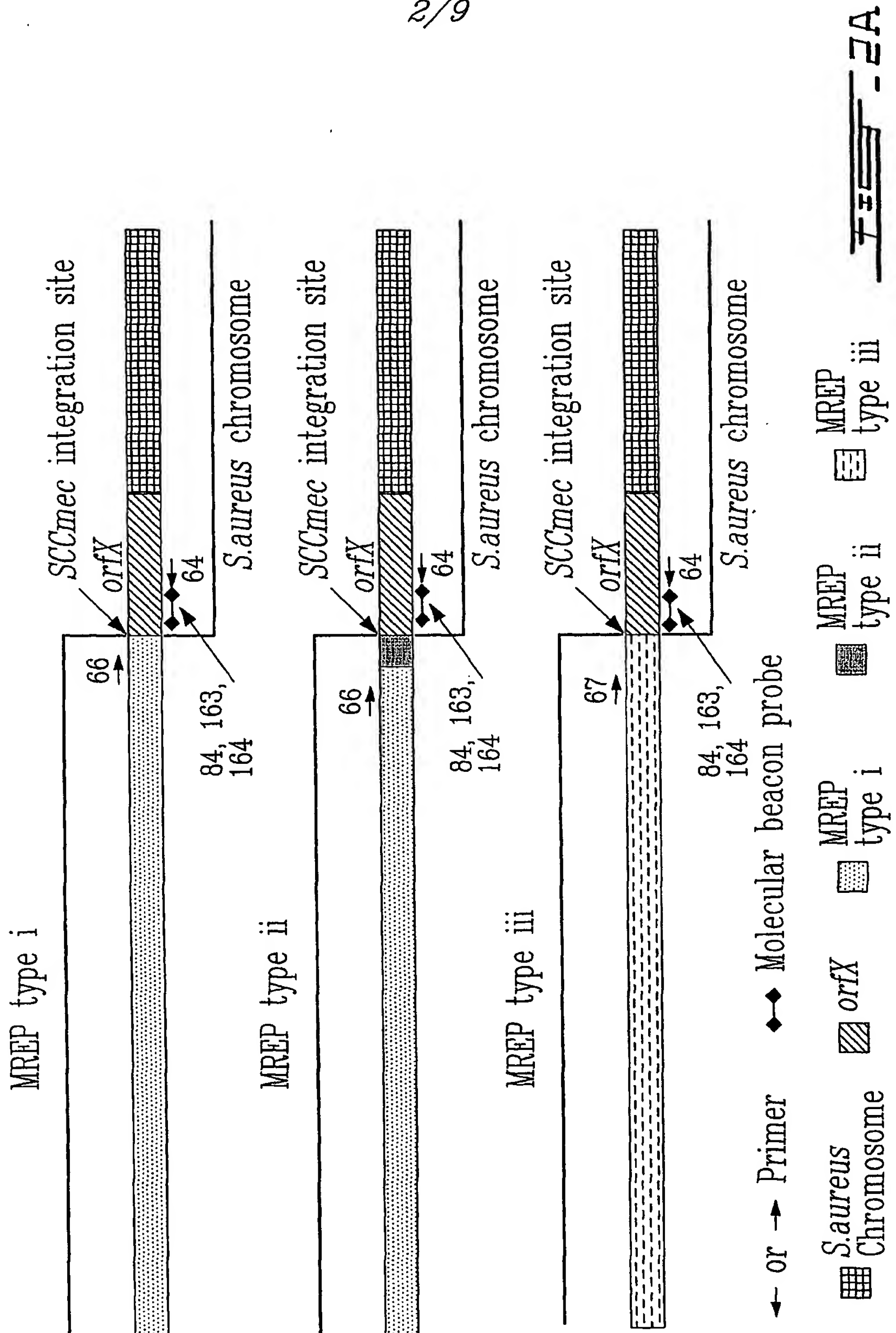
10

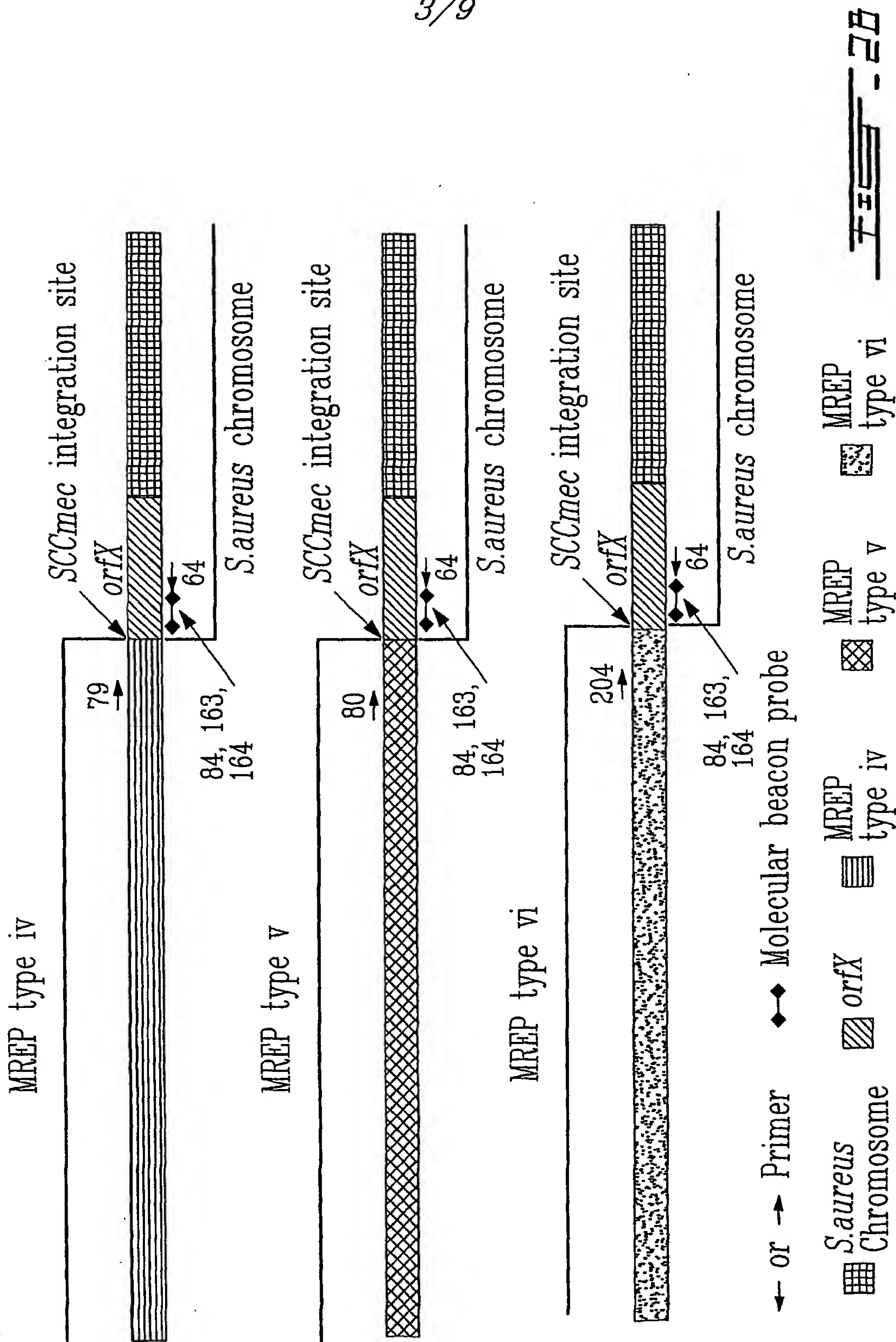
20. The composition of claim 18, which further comprises probes, which SEQ ID NOs are: 32, 83, 84, 160, 161, 162, 163, 164.

15

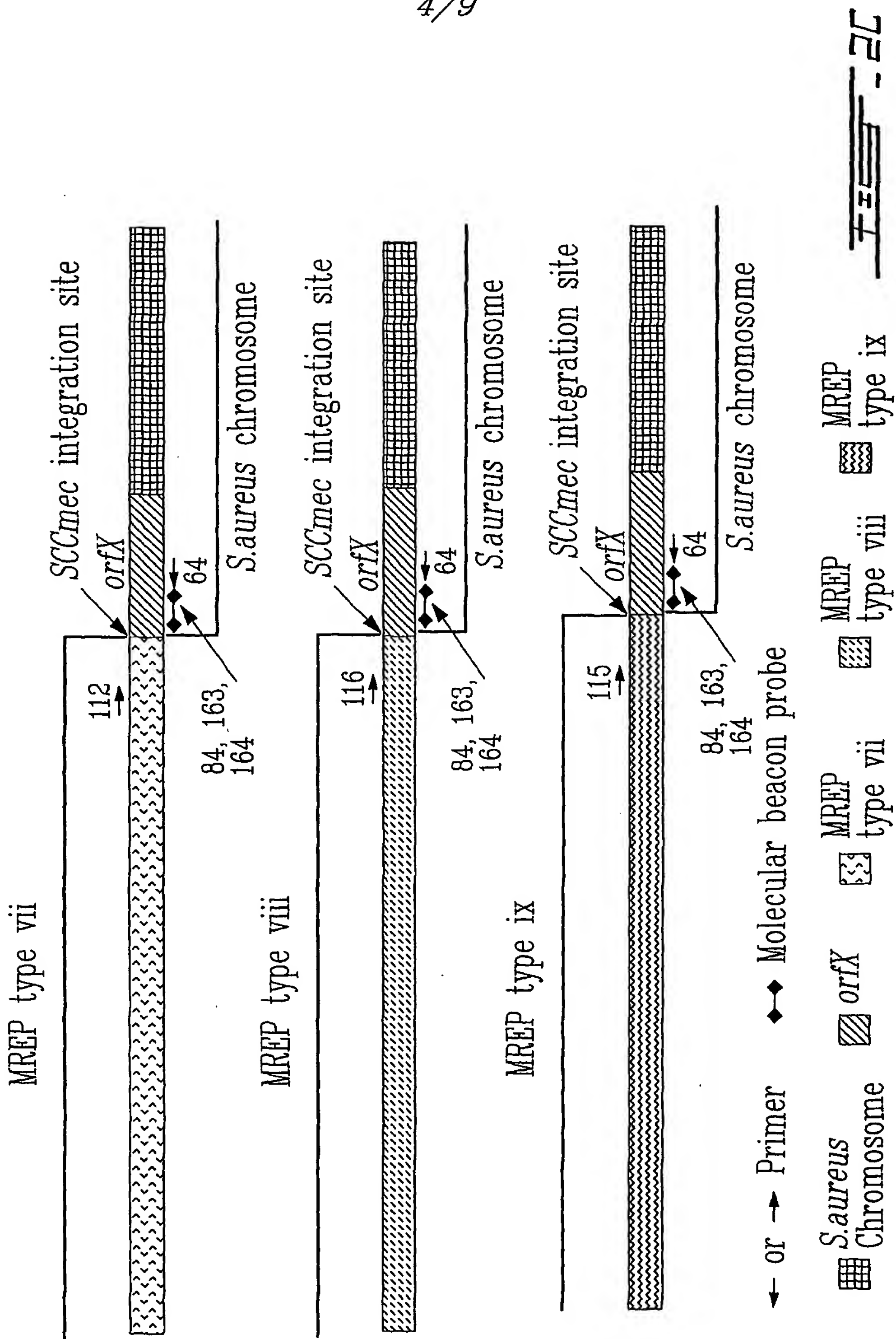


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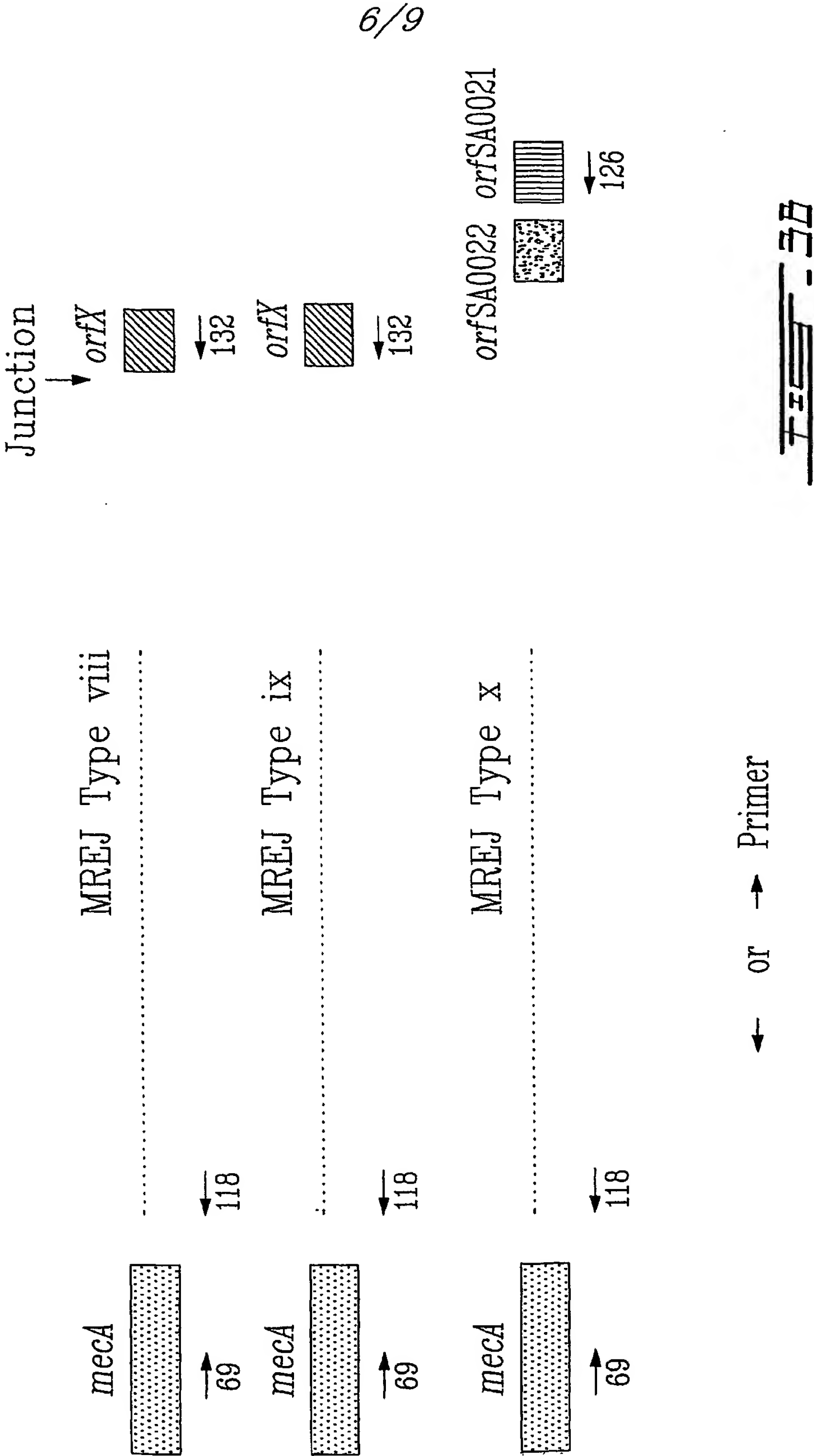


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| | | | | | | | | | | |
|------------|-------------|-------------|------------|--------------|-------------|-------------|------------|-------------|-------------|--------------|
| Type iii | ATGAGACCTAC | ATTTAAATTA | ACATATTGAT | GAAAGAAAT | TTTAAATTTAA | ACTAATGGAA | TCAAGATAGA | ATGAAAGGAA | ATATTCATATG | CCATACGATT |
| Type vii | ATCTAATATA | ATTTGTGAGG | AATGATTACG | ATATCTAGCTTA | ACCGGCTAAAT | GAAATTTT | AAGTACATA | CTTAGACATA | TTTTCATT | AGTAAATTT |
| Type vi | AAAGAAAGAC | GGTGAGCG | GCATACGAC | AGATAGCTAT | TACTGTTTT | CATACAGCT | AAAGCTAAAT | CTTAAATAG | TTTTCGTC | GTATATTTGT |
| Type i | TCTGAAATAC | TTTATACGAA | GGAAATCTCT | AGCTTTGACA | AAATTCATTC | TGCATCTTAA | TATAGTAAAT | TACCGGTAAAT | TAATANAATAG | TATCATATTCGA |
| Type ii | TACCTAATAC | TTTATAGCGAA | GGAAATCTCT | AGCTTTGACA | AAATTCATTC | TGCATCTTAA | TATAGTAAAT | TACCGGTAAAT | TAATANAATAG | TATCATATTCGA |
| Type ix | AAACAAAGATT | ATGCTTAGCG | TCAATATATG | GCTTATCAAA | GTGAATATGC | ATTCGAAAT | GAAGTACTTC | AAACAATCTGA | GGAAATTCAGC | TAATGAAAGAG |
| Type viiii | ACTTCANCTT | TGAAGGGAAT | AAATTAGGAA | CTTATTTATA | TTTATCTT | ATCTCATTTAA | TATCTATTTT | TTTATTAATA | ATATTAATAA | TAATTAATATC |
| Type v | TAGTGTATAT | AACTAATGAG | TTCTATCTAT | AACCTGCTTT | TTTCAATCG | CATCAGTA | AAGGATGTAG | AGATTGTG | GAAATTTCT | TCCGATGTTT |
| Type iv | AGAATATGAT | TATTAATTTA | CTATTATTT | TTTAAATATTA | AAAGCAAGATA | TGAATATTT | ATTCATATCC | TCACCTTC | AAATATTTAGT | TTTCAATTCGA |

bits

Position

Type iii: ATAAAGCA

Type vii: TGAATTAC

Type vi: GGTATTCATA

Type i: AGAAATACG

Type ii: AGAAATACG

Type ix: TAAATATAC

Type viii: TTTAGAAAG

Type v: TTAATATAT

Type iv: ATATTTAGAT

734 48

| | | | | | | | | | | | | |
|-----------|-----|-------------|-------------|-------------|------------|-------------|-------------|------------|------------|------------|------------|-----|
| Type iii | 401 | GGTAAAG...T | AGTTTCACCGT | TAATAGTACAA | AATTTGGGAG | CTATCCCTAA | ATTAAGCAATA | SAGCAATTGA | ATTCGACCGT | AAAAGTGTG | AGGTATGTG | 500 |
| Type vii | | ATAAGAGCTA | ACTTAAACGT | AGCAAGCTAG | TTTATATGAT | TTTAAATAG | TTTAAATAT | GTGAGCTTT | TTTAAAGCA | CAATTTATG | AACATATG | |
| Type vi | | GCGTAACGAA | TTAAAGTAA | TTAATATTA | ATAGGCAAG | ATAACAGTAA | AATGAGCTGG | CTTTACAGCT | TTCAAATGCT | ATTTATTTAA | TCATATTTAA | |
| Type i | | GGTTCGTAAT | AAATCTGCA | GGGTATAGG | TTGATCTAAT | ATAATCTTAA | TCCATGCTAA | CTGTTAAAG | CTGTTAAAG | TGCATTAATA | AGACCTAATA | |
| Type ii | | GGTACCTTAA | AAATCTGCA | GGGTATAGG | TTGATCTAAT | ATAATCTTAA | TCCATGCTAA | CTGTTAAAG | CTGTTAAAG | TGCATTAATA | AGACCTAATA | |
| Type ix | | CTGACCTTTGA | TTGACCTTTGA | AAATTAAGGA | AATTTAGGCT | CTGACCTTTGA | TTGACCTTTGA | CTGTTAAAG | CTGTTAAAG | TGCATTAATA | AGACCTAATA | |
| Type viii | | TAAGTAGGCT | CTGACCTTTGA | AAATTAAGGA | AATTTAGGCT | CTGACCTTTGA | TTGACCTTTGA | CTGTTAAAG | CTGTTAAAG | TGCATTAATA | AGACCTAATA | |
| Type v | | ATTAAATTTGA | CACTTAAAT | AAATTAAGGA | AATTTAGGCT | CTGACCTTTGA | TTGACCTTTGA | CTGTTAAAG | CTGTTAAAG | TGCATTAATA | AGACCTAATA | |
| Type iv | | CCCTAAATCA | CACTTAAAT | AAATTAAGGA | AATTTAGGCT | CTGACCTTTGA | TTGACCTTTGA | CTGTTAAAG | CTGTTAAAG | TGCATTAATA | AGACCTAATA | |

FIG. 4C

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS:

HULETSKY, Ann ¹, 1231 Av des Pins', Sillery, Quebec,
Canada, G1S 4J3

ROSSBACH, Valery ¹, 55 Rue du Sauternes, Aylmer,
Quebec, Canada, J9H 3W7

¹:Canadian citizenship

(ii) TITLE OF THE INVENTION: SEQUENCES FOR DETECTION AND
IDENTIFICATION OF METHICILLIN-RESISTANT STAPHYLOCOCCUS
AUREUS

(iii) NUMBER OF SEQUENCES: 233

(iv) CORRESPONDENCE ADDRESS:

| | |
|-----|------------|
| (A) | ADDRESSEE: |
| (B) | STREET: |
| (C) | CITY: |
| (D) | STATE: |
| (E) | COUNTRY: |
| (F) | ZIP: |

(v) COMPUTER READABLE:

| | |
|-----|--------------|
| (A) | MEDIUM TYPE: |
| (B) | COMPUTER: |
| (C) | OPERATING: |
| (D) | SOFTWARE: |

(vi) CURRENT APPLICATION DATA:

| | |
|-----|-----------------|
| (A) | APPLICATION: |
| (B) | FILING DATE: |
| (C) | CLASSIFICATION: |

(vii) PRIOR APPLICATION DATA:

| | |
|-----|--------------|
| (A) | APPLICATION: |
| (B) | FILING DATE: |

(viii) ATTORNEY/AGENT INFORMATION:

(A)

NAME:

(B)

REGISTRATION NUMBER:

(ix) TELECOMMUNICATION INFORMATION:

(A)

TELEPHONE:

(B)

TELEFAX:

2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3050 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 10442
- (C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

| | | | | | |
|-------------|------------|------------|------------|-------------|------|
| TCGTGCCATT | GATGCAGAGG | GACATACATT | AGATATTTGG | TTGCGTAAGC | 50 |
| AACGAGATAA | TCATTCAGCA | TATGCGTTTA | TCAAACGTCT | CATTAAACAA | 100 |
| TTTGGTAAAC | CTCAAAAGGT | AATTACAGAT | CAGGCACCTT | CAACGAAGGT | 150 |
| AGCAATGGCT | AAAGTAATTA | AAGCTTTTAA | ACTTAAACCT | GACTGTCATT | 200 |
| GTACATCGAA | ATATCTGAAT | AACCTCATTG | AGCAAGATCA | CCGTCATATT | 250 |
| AAAGTAAGAA | AGACAAGGTA | TCAAAGTATC | AATACAGCAA | AGAATACTTT | 300 |
| AAAAGGTATT | GAATGTATTT | ACGCTCTATA | TAAAAAGAAC | CGCAGGTCTC | 350 |
| TTCAGATCTA | CGGATTTTCG | CCATGCCACG | AAATTAGCAT | CATGCTAGCA | 400 |
| AGTTAAGCGA | ACACTGACAT | GATAAATTAG | TGGTTAGCTA | TATTTTTTTA | 450 |
| CTTTGCAACA | GAACCGAAAA | TAATCTCTTC | AATTTATTTT | TATATGAATC | 500 |
| CTGTGACTCA | ATGATTGTAA | TATCTAAAGA | TTTCAGTTCA | TCATAGACAA | 550 |
| TGTTCTTTTC | AACATTTTTT | ATAGCAAATT | GATTAAATAA | ATTCTCTAAT | 600 |
| TTCTCCCGTT | TGATTTCACT | ACCATAGATT | ATATTATCAT | TGATATAGTC | 650 |
| AATGAATAAT | GACAAATTAT | CACTCATAAC | AGTCCCAACC | CCTTTATTTT | 700 |
| GATAGACTAA | TTATCTTCAT | CATTGTAAAA | CAAATTACAC | CCTTTAAATT | 750 |
| TAACTCAACT | TAAATATCGA | CAAATTAAAA | AACAATAAAA | TTACTTGAAT | 800 |
| ATTATTCATA | ATATATTAAC | AACTTTATTA | TACTGCTCTT | TATATATAAA | 850 |
| ATCATTAATA | ATTAAACAAG | CCTTAAATAA | TTTAACTTTT | TTGTGATTAT | 900 |
| TACACATTAT | CTTATCTGCT | CTTTATCACC | ATAAAAATAG | AAAAACAAG | 950 |
| ATTCCTAAAG | AATATAGGAA | TCTTGTTTCA | GACTGTGGAC | AAACTGATTT | 1000 |
| TTTATCAGTT | AGCTTATTTA | GAAAGTTTTA | TTTAAATTAC | AGTTTCTATT | 1050 |
| TTTATTAGAT | CACAATTTTA | TTTTAGCTCT | TGTTCAAGTA | ATCATTTTTC | 1100 |
| GCCAAAAACT | TTATACTGAA | TAGCTTCTAC | ATTAAATACT | TTGTCAATGA | 1150 |
| GATCATCTAC | ATCTTTAAAT | TCAGAATAAT | TTGCATATGG | ATCTATAAAA | 1200 |
| TAAAATTGTG | GTTCTTTACC | GGAAACATTA | AATATTCTTA | ATATTAAATA | 1250 |
| TTTCTGCTTA | TATTCTTTCA | TAGCAAACAT | TTCATTTAGC | GACATAAAAA | 1300 |
| ATGGTTCCTC | AATACTAGAA | GATGTAGATG | TTTTAATTTC | AATAAATTTT | 1350 |
| TCTACAGCTT | TATCTGTATT | TGTTGGATCA | AAAGCTACTA | AATCATAGCC | 1400 |
| ATGACCGTGT | TGAGAGCCTG | GATTATCATT | TAAAATATTC | CTAAACTGTT | 1450 |
| CTTTCCTTATC | TTCGTCTATT | TTATTATCAA | TTAGCTCATT | AAAGTAATTT | 1500 |
| AGCGCTAATT | TTTCTCCAAC | TTTACCGGTT | AATTTATTCT | CTTTATTTGA | 1550 |
| TTTTTCAATT | TCTGAATCAT | TTTTAGTAGT | CTTTGATACA | CCTTTTTTTAT | 1600 |
| ATTTTGAAT | TATTCCTTTA | GGTGCTTCCA | CTTCCTTGAG | TGTCTTATCT | 1650 |
| TTTTGTGCTG | TTCTAATTTT | TTCAATTTTC | CTGTCTTCCT | GTATTTTCGTC | 1700 |
| TATGCTATTG | ACCAAGCTAT | CATAGGATGT | TTTTGTAACT | TTTGAAGCTA | 1750 |

| | | | | | |
|-------------|------------|-------------|------------|------------|------|
| ATTCATTAAA | TAGTTCTAAA | AATTTCTTTA | AATCCTCTAG | CATATCTTCT | 1800 |
| TCTGTGAATC | CTTCATTCAA | ATCATAATAT | TTGAATCTTA | TTGATCCATG | 1850 |
| AGAATATCCT | GATGGATAAT | CATTTTTTTAA | ATCATAAGAT | GAATCTTTAT | 1900 |
| TTTCTGCGTA | ATAAAATCTT | CCAGTATTAA | ATTCATTTGA | TGTAATATAT | 1950 |
| TTATTGAGTT | CGGAAGATAA | AGTTAATGCT | CTTTGTTTTG | CAGCATTTTT | 2000 |
| ATCCCGCGGA | AACATATCAC | TTATCTTTGA | CCATCCTTGA | TTCAAAGATA | 2050 |
| AGTATATGCC | TTCTCCTTCC | GGATGAAAAA | GATATACCAA | ATAATATCCA | 2100 |
| TCCTTTGTTT | CTTTTGTTAT | ATTCTCATCA | TATATTGAAA | TCCAAGGAAC | 2150 |
| TTTACTATAG | TTCCCAGTAG | CAACCTTCCC | TACAACTGAA | TATTTATCTT | 2200 |
| CTTTTATATG | CACTTTTAAC | TGCTTGGGTA | ACTTATCATG | GACTAAAGTT | 2250 |
| TTATATAGAT | CACCTTTATC | CCAATCAGAT | TTTTTAACTA | CATTATTGGT | 2300 |
| ACGTTTCTCT | TTAATTAATT | TAAGGACCTG | CATAAAGTTG | TCTATCATTT | 2350 |
| GAAATTCCCT | CCTATTATAA | AATATATTAT | GTCTCATTTT | CTTCAATATG | 2400 |
| TACTTATTTA | TATTTTACCG | TAATTTACTA | TATTTAGTTG | CAGAAAGAAT | 2450 |
| TTTCTCAAAG | CTAGAACTTT | GCTTCACTAT | AAGTATTCAG | TATAAAGAAT | 2500 |
| ATTTGCTAT | TATTTACTTG | AAATGAAAGA | CTGCGGAGGC | TAACTATGTC | 2550 |
| AAAAATCATG | AACCTCATTA | CTTATGATAA | GCTTCTCCTC | GCATAATCTT | 2600 |
| AAATGCTCTG | TACACTTGTT | CAATTAACAC | AACCCGCATC | ATTTGATGTG | 2650 |
| GGAATGTCAT | TTTGCTGAAT | GATAGTGCGT | AGTTACTGCG | TTGTAAGACG | 2700 |
| TCCTTG TGCA | GGCCGTTTGA | TCCGCCAATG | ACGAAAACAA | AGTCGCTTTG | 2750 |
| CCCTTGGGTC | ATGCGTTGGT | TCAATTCTTG | GGCCAATCCT | TCGGAAGATA | 2800 |
| GCATCTTTCC | TTGTATTTCT | AATGTAATGA | CTGTGGATTG | TGGTTTGATT | 2850 |
| TTGGCTAGTA | TTCGTTGGCC | TTCTTTTTTCT | TTTACTTGCT | CAATTTCTTT | 2900 |
| GTCACTCATA | TTTTCTGGTG | CTTTTTTCGTC | TGGAACCTCT | ATGATGTCTA | 2950 |
| TCTTG GTGTA | TGGGCCTAAA | CGTTTTTTCAT | ATTCTGCTAT | GGCTTGCTTC | 3000 |
| CAATATTTCT | CTTTTAGTTT | CCCTACAGCT | AAAATGGTGA | TTTTCATGTC | 3050 |

2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3050 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: N315
- (C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

| | | | | | |
|------------|------------|-------------|------------|------------|-----|
| ACCTCATTGA | GCAAGATCAC | CGTCATATTA | AAGTAAGAAA | GACAAGGTAT | 50 |
| CAAAGTATCA | ATACAGCAAA | GAATACTTTA | AAAGGTATTG | AATGTATTTA | 100 |
| CGCTCTATAT | AAAAAGAACC | GCAGGTCTCT | TCAGATCTAC | GGATTTTCGC | 150 |
| CATGCCACGA | AATTAGCATC | ATGCTAGCAA | GTTAAGCGAA | CACTGACATG | 200 |
| ATAAATTAGT | GGTTAGCTAT | ATTTTTTTTAC | TTTGCAACAG | AACCGAAAAT | 250 |
| AATCTCTTCA | ATTTATTTTT | ATATGAATCC | TGTGACTCAA | TGATTGTAAT | 300 |

| | | | | | |
|------------|-------------|-------------|-------------|-------------|------|
| ATCTAAAGAT | TTCAGTTCAT | CATAGACAAT | GTTCTTTTCA | ACATTTTTTA | 350 |
| TAGCAAATTG | ATTAAATAAA | TTCTCTAATT | TCTCCCGTTT | GATTTCACTA | 400 |
| CCATAGATTA | TATTATCATT | GATATAGTCA | ATGAATAATG | ACAAATTATC | 450 |
| ACTCATAACA | GTCCCAACCC | CTTTCTTTTG | ATAGACTAAT | TATCTTCATC | 500 |
| ATTGTAAAAC | AAATTACACC | CTTTAAATTT | AACTCAACTT | AAATATCGAC | 550 |
| AAATTAAAAA | ACAATAAAAT | TACTTGAATA | TTATTCATAA | TATATTAACA | 600 |
| ACTTTATTAT | ACTGCTCTTT | ATATATAAAA | TCATTAATAA | TTAAACAAGC | 650 |
| CTTAAAATAT | TTAACTTTTT | TGTGATTATT | ACACATTATC | TTATCTGCTC | 700 |
| TTTATCACCA | TAAAAATAGA | AAAAACAAGA | TTCCTAAAGA | ATATAGGAAT | 750 |
| CTTGTTTCAG | ACTGTGGACA | AACTGATTTT | TTATCAGTTA | GCTTATTTAG | 800 |
| AAAGTTTTAT | TTAAATTACA | GTTTCTATTT | TTATTAGATC | ACAATTTTAT | 850 |
| TTTAGCTCTT | GTTCAAGTAA | TCATTTTTTCG | CCAAAAACTT | TATACTGAAT | 900 |
| AGCTTCTACA | TTAAATACTT | TGTCAATGAG | ATCATCTACA | TCTTTAAATT | 950 |
| CAGAATAATT | TGCATATGGA | TCTATAAAAT | AAAATTGTGG | TTCTTTACCG | 1000 |
| GAAACATTAA | ATATTCTTAA | TATTAAATAT | TTCTGCTTAT | ATTCTTTCAT | 1050 |
| AGCAAACATT | TCATTTAGCG | ACATAAAAAA | TGGTTCCTCA | ATACTAGAAG | 1100 |
| ATGTAGATGT | TTTAATTTCA | ATAAATTTTT | CTACAGCTTT | ATCTGTATTT | 1150 |
| GTTGGATCAA | AAGCTACTAA | ATCATAGCCA | TGACCGTGTT | GAGAGCCTGG | 1200 |
| ATTATCATTT | AAAATATTCC | TAAACTGTTC | TTTCTTATCT | TCGTCTATTT | 1250 |
| TATTATCAAT | TAGCTCATT | AAGTAATTTA | GCGCTAATTT | TTCTCCAAC | 1300 |
| TTACCGGTTA | ATTTATTCTC | TTTATTTGAT | TTTTCAATTT | CTGAATCATT | 1350 |
| TTTAGTAGTC | TTTGATACAC | CTTTTTTTATA | TTTTGGAATT | ATTCCTTTAG | 1400 |
| GTGCTTCCAC | TTCTTGAGT | GTCTTATCTT | TTTGTGCTGT | TCTAATTTCT | 1450 |
| TCAATTTTCG | TGTCTTCCTG | TATTTCTGCT | ATGCTATTGA | CCAAGCTATC | 1500 |
| ATAGGATGTT | TTTGTAACCT | TTGAAGCTAA | TTCAATTAAAT | AGTTCTAAAA | 1550 |
| ATTTCTTTAA | ATCCTCTAGC | ATATCTTCTT | CTGTGAATCC | TTCAATTCAAA | 1600 |
| TCATAATATT | TGAATCTTAT | TGATCCATGA | GAATATCCTG | ATGGATAATC | 1650 |
| ATTTTTTTAA | TCATAAGATG | AATCTTTATT | TTCTGCGTAA | TAAAATCTTC | 1700 |
| CAGTATTAAA | TTCAATTTGAT | GTAATATATT | TATTGAGTTC | GGAAGATAAA | 1750 |
| GTTAATGCTC | TTTGTTTTGC | AGCATTTTTTA | TCCCGCGGAA | ACATATCACT | 1800 |
| TATCTTTGAC | CATCCTTGAT | TCAAAGATAA | GTATATGCCT | TCTCCTTCCG | 1850 |
| GATGAAAAAG | ATATACCAAA | TAATATCCAT | CCTTTGTTTC | TTTTGTTATA | 1900 |
| TTCTCATCAT | ATATTGAAAT | CCAAGGAACT | TTACTATAGT | TCCCAGTAGC | 1950 |
| AACCTTCCCT | ACAACCTGAAT | ATTTATCTTC | TTTTATATGC | ACTTTTAACT | 2000 |
| GCTTGGGTAA | CTTATCATGG | ACTAAAGTTT | TATATAGATC | ACCTTTATCC | 2050 |
| CAATCAGATT | TTTTAACTAC | ATTATTGGTA | CGTTTCTCTT | TAATTAATTT | 2100 |
| AAGGACCTGC | ATAAAGTTGT | CTATCATTTG | AAATTCCTCT | CTATTATAAA | 2150 |
| ATATATTATG | TCTCATTTTC | TTCAATATGT | ACTTATTTAT | ATTTTACCGT | 2200 |
| AATTTACTAT | ATTTAGTTGC | AGAAAGAATT | TTCTCAAAGC | TAGAACTTTG | 2250 |
| CTTCACTATA | AGTATTCAGT | ATAAAGAATA | TTTCGCTATT | ATTTACTTGA | 2300 |
| AATGAAAGAC | TGCGGAGGCT | AACTATGTCA | AAAATCATGA | ACCTCATTAC | 2350 |
| TTATGATAAG | CTTCTTAAAA | ACATAACAGC | AATTCACATA | AACCTCATAT | 2400 |
| GTTCTGATAC | ATTCAAAATC | CCTTTATGAA | GCGGCTGAAA | AAACCGCATC | 2450 |
| ATTTATGATA | TGCTTCTCCA | CGCATAATCT | TAAATGCTCT | ATACACTTGC | 2500 |
| TCAATTAACA | CAACCCGCAT | CATTTGATGT | GGGAATGTCA | TTTTGCTGAA | 2550 |
| TGATAGTGCG | TAGTTACTGC | GTTGTAAGAC | GTCCTTGTGC | AGGCCGTTTG | 2600 |
| ATCCGCCAAT | GACGAATACA | AAGTCGCTTT | GCCCTTGGGT | CATGCGTTGG | 2650 |
| TTCAATTCTT | GGGCCAATCC | TTCGGAAGAT | AGCATCTTTC | CTTGTATTTT | 2700 |
| TAATGTAATG | ACTGTGGATT | GTGGTTTAAT | TTTGGCTAGT | ATTCGTTGGC | 2750 |
| CTTCTTTTTT | TTTTACTTGC | TCAATTTCTT | TGTCGCTCAT | ATTTTCTGGT | 2800 |
| GCTTTTTTCG | CTGGAACCTC | TATGATGTCT | ATCTTGGTGT | ATGGGCCTAA | 2850 |
| ACGTTTTTCA | TATTCTGCTA | TGGCTTGCTT | CCAATATTTT | TCTTTTAGTT | 2900 |

| | | | | | |
|------------|------------|------------|------------|------------|------|
| TCCCTACAGC | TAAAATGGTG | ATTTTCATGT | CGTTTGGTCC | TCCAAATTGT | 2950 |
| TATCAACTTT | CCAGTTATCC | ACAAGTTATT | AACTTGTTCA | CACTGTTCCC | 3000 |
| TCTTATTATA | CCAATATTTT | TTGCAGTTT | TGATATTTTC | CTGACATTTA | 3050 |

2) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3183 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 8325
- (C) ACCESSION NUMBER: AB014440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

| | | | | | |
|-------------|------------|------------|-------------|------------|------|
| CTGCAGAGGT | AATTATTCCA | AACAATACCA | TTGATTTC | AGGAGAAAGA | 50 |
| GATGACGTTA | GAACGCGTGA | AACAAATTTA | GGAAACGCGA | TTGCAGATGC | 100 |
| TATGGAAGCG | TATGGCGTTA | AGAATTTCTC | TAAAAAGACT | GACTTTGCCG | 150 |
| TGACAAATGG | TGGAGGTATT | CGTGCCTCTA | TCGCAAAAGG | TAAGGTGACA | 200 |
| CGCTATGATT | TAATCTCAGT | ATTACCATTT | GGAAATACGA | TTGCGCAAAT | 250 |
| TGATGTAAAA | GGTTCAGACG | TCTGGACGGC | TTTCGAACAT | AGTTTAGGCG | 300 |
| CACCAACAAC | ACAAAAGGAC | GGTAAGACAG | TGTTAACAGC | GAATGGCGGT | 350 |
| TTACTACATA | TCTCTGATTC | AATCCGTGTT | TACTATGATA | TAAATAAACC | 400 |
| GTCTGGCAAA | CGAATTAATG | CTATTCAAAT | TTTAAATAAA | GAGACAGGTA | 450 |
| AGTTTGAAAA | TATTGATTTA | AAACGTGTAT | ATCACGTAAC | GATGAATGAC | 500 |
| TTACACAGCAT | CAGGTGGCGA | CGGATATAGT | ATGTTTCGGTG | GTCCTAGAGA | 550 |
| AGAAGGTATT | TCATTAGATC | AAGTACTAGC | AAGTTATTTA | AAAACAGCTA | 600 |
| ACTTAGCTAA | GTATGATACG | ACAGAACCAC | AACGTATGTT | ATTAGGTAAA | 650 |
| CCAGCAGTAA | GTGAACAACC | AGCTAAAGGA | CAACAAGGTA | GCAAAGGTAG | 700 |
| TAAGTCTGGT | AAAGATACAC | AACCAATTGG | TGACGACAAA | GTGATGGATC | 750 |
| CAGCGAAAAA | ACCAGCTCCA | GGTAAAGTTG | TTTTGTTGCT | AGCGCATAGA | 800 |
| GGAAGTGTTA | GTAGCGGTAC | AGAAGGTTCT | GGTCGCACAA | TAGAAGGAGC | 850 |
| TACTGTATCA | AGCAAGAGTG | GGAAACAATT | GGCTAGAATG | TCAGTGCCTA | 900 |
| AAGGTAGCGC | GCATGAGAAA | CAGTTACCAA | AAACTGGAAC | TAATCAAAGT | 950 |
| TCAAGCCCAG | AAGCGATGTT | TGTATTATTA | GCAGGTATAG | GTTTAATCGC | 1000 |
| GACTGTACGA | CGTAGAAAAG | CTAGCTAAAA | TATATTGAAA | ATAATACTAC | 1050 |
| TGTATTTCTT | AAATAAGAGG | TACGGTAGTG | TTTTTTTATG | AAAAAAAGCG | 1100 |
| ATAACCGTTG | ATAAATATGG | GATATAAAAA | CGAGGATAAG | TAATAAGACA | 1150 |
| TCAAGGTGTT | TATCCACAGA | AATGGGGATA | GTTATCCAGA | ATTGTGTACA | 1200 |
| ATTTAAAGAG | AAATACCCAC | AATGCCCACA | GAGTTATCCA | CAAATACACA | 1250 |
| GGTTATACAC | TAAAAATCGG | GCATAAATGT | CAGGAAAATA | TCAAAAAC | 1300 |
| CAAAAAATAT | TGGTATAATA | AGAGGGAACA | GTGTGAACAA | GTTAATAACT | 1350 |
| TGTGGATAAC | TGGAAAGTTG | ATAACAATTT | GGAGGACCAA | ACGACATGAA | 1400 |
| AATCACCATT | TTAGCTGTAG | GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | 1450 |

| | | | | | |
|------------|------------|-------------|-------------|------------|------|
| CCATAGCAGA | ATATGAAAAA | CGTTTAGGCC | CATACACCAA | GATAGACATC | 1500 |
| ATAGAAGTTC | CAGACGAAAA | AGCACCAGAA | AATATGAGTG | ACAAAGAAAT | 1550 |
| TGAGCAAGTA | AAAGAAAAAG | AAGGCCAACG | AATACTAGCC | AAAATCAAAC | 1600 |
| CACAATCCAC | AGTCATTACA | TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | 1650 |
| GAAGGATTGG | CCCAAGAATT | GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | 1700 |
| CTTTGTTTTC | GTCATTGGCG | GATCAAACGG | CCTGCACAAG | GACGTCTTAC | 1750 |
| AACGCAGTAA | CTACGCACTA | TCATTTCAGCA | AAATGACATT | CCCACATCAA | 1800 |
| ATGATGCGGG | TTGTGTTAAT | TGAACAAGTG | TACAGAGCAT | TTAAGATTAT | 1850 |
| GCGAGGAGAG | GCGTATCATA | AGTAAACTA | AAAAATTCTG | TATGAGGAGA | 1900 |
| TAATAATTTG | GAGGGTGTTA | AATGGTGGAC | ATTAAATCCA | CGTTCATTCA | 1950 |
| ATATATAAGA | TATATCACGA | TAATTGCGCA | TATAACTTAA | GTAGTAGCTA | 2000 |
| ACAGTTGAAA | TTAGGCCCTA | TCAAATTGGT | TTATATCTAA | AATGATTAAT | 2050 |
| ATAGAATGCT | TCTTTTTGTC | CTTATTAAAT | TATAAAAGTA | ACTTTGCAAT | 2100 |
| AGAAACAGTT | ATTCATAAT | CAACAGTCAT | TGACGTAGCT | AAGTAATGAT | 2150 |
| AAATAATCAT | AAATAAAATT | ACAGATATTG | ACAAAAATA | GTAAATATTC | 2200 |
| CAATGAAGTT | TCAAAAGAAC | AATTCCAAGA | AATTGAGAAT | GTAAATAATA | 2250 |
| AGGTCAAAGA | ATTTTATTAA | GATTTGAAAG | AGTATCAATC | AAGAAAGATG | 2300 |
| TAGTTTTTTA | ATAAACTATT | TGGAAAATAA | TTATCATAAT | TTAAAAACTG | 2350 |
| ACAATTTGCG | AGACTCATAA | AATGTAATAA | TGGAAATAGA | TGTAAAATAT | 2400 |
| AATTAAGGGG | TGTAATATGA | AGATTAATAT | TTATAAATCT | ATTTATAATT | 2450 |
| TTCAGGAAAC | AAATACAAAT | TTTTTAGAGA | ATCTAGAATC | TTTAAATGAT | 2500 |
| GACAATTATG | AACTGCTTAA | TGATAAAGAA | CTTGTTAGTG | ATTCAAATGA | 2550 |
| ATTAAAATTA | ATTAGTAAAG | TTTATATACG | TAAAAAAGAC | AAAAAACTAT | 2600 |
| TAGATTGGCA | ATTATTAATA | AAGAATGTAT | ACCTAGATAC | TGAAGAAGAT | 2650 |
| GACAATTTAT | TTTCAGAATC | CGGTCATCAT | TTTGATGCAA | TATTATTTCT | 2700 |
| CAAAGAAGAT | ACTACATTAC | AAAATAATGT | ATATATTATA | CCTTTTGGAC | 2750 |
| AAGCATATCA | TGATATAAAT | AATTTGATTG | ATTATGACTT | CGGAATTGAT | 2800 |
| TTTGCAGAAA | GAGCAATCAA | AAATGAAGAC | ATAGTTAATA | AAAATGTTAA | 2850 |
| TTTTTTTCAA | CAAAACAGGC | TTAAAGAGAT | TGTTAATTAT | AGAAGGAATA | 2900 |
| GTGTAGATTA | CGTTAGACCT | TCAGAATCTT | ATATATCAGT | CCAAGGACAT | 2950 |
| CCACAGAATC | CTCAAATTTT | TGGAAAAACA | ATGACTTGTTG | GTACAAGTAT | 3000 |
| TTCATTGCGT | GTACCGAATA | GAAAGCAGCA | ATTCATAGAT | AAAATTAGTG | 3050 |
| TGATAATCAA | AGAAATAAAC | GCTATTATTA | ATCTTCCTCA | AAAAATTAGT | 3100 |
| GAATTTCTTA | GAATAGTAAC | TTTAAAGAC | TTGAATAAAA | TAGAAGTATT | 3150 |
| AGATACTTTA | TTGCTAAAAA | AACTATCGAA | TTC | | 3183 |

2) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: 86/560
- (C) ACCESSION NUMBER: AB013471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACA | | | 479 |

2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 86/961
- (C) ACCESSION NUMBER: AB013472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATAAC | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACAG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: 85/3907

(C) ACCESSION NUMBER: AB013473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATCCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTGTGT | TAGAAACAGT | | | 480 |

2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: 86/2652

(C) ACCESSION NUMBER: AB013474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATCCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACAG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/1340
- (C) ACCESSION NUMBER: AB013475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

| | | | | | |
|------------|------------|------------|------------|-------------|-----|
| GGCGGATCAA | ACGGCCTGCA | CAAGGACGTC | TTACAACGCA | GTAAC TACGC | 50 |
| ACTATCATT | AGCAAAATGA | CATTCCCACA | TCAAATGATG | CGGGTTGTGT | 100 |
| TAATTGAACA | AGTGTACAGA | GCATTTAAGA | TTATGCGTGG | AGAAGCGTAT | 150 |
| CATAAATAAA | ACTAAAAATT | AGGTTGTGTA | TAATTTAAAA | ATCTAATGAG | 200 |
| ATGTGGAGGA | ATTACATATA | TGAAATATTG | GATTATNCCT | TGCAATATCA | 250 |
| TACGATGTTT | ATAGAGTGTT | TAATAAACCA | TTTTTCAACT | ATTGATGATC | 300 |
| TACAATATA | | | | | 309 |

2) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/1762
- (C) ACCESSION NUMBER: AB013476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTGGCGGATC | AAACGGCCTG | CACAAGGACG | TCTTACAACG | CAGTAACTAC | 50 |
| GCACTATCAT | TCAGCAAAAT | GACATTCCCA | CATCAAATGA | TGCGGGTTGT | 100 |
| GTTAATTGAA | CAAGTGTACA | GAGCATTTAA | GATTATGCGT | GGAGAAGCGT | 150 |
| ATCATAAATA | AAACTAAAAA | TTAGGTTGTG | TATAATTTAA | AAATTTAATG | 200 |
| AGATGTGGAG | GAATTACATA | TATGAAATAT | TGGATTATAC | CTTGCAATAT | 250 |
| CATACGATGT | TTATAGAGTG | TTTAATAAAC | CATTTTTCOA | CTATTGATGA | 300 |

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TCTAGAATAT | ATAATAACTG | TACAAATTAT | ATTGATTATG | GAACTACAAT | 350 |
| TAAATTAAGA | AATTGATGAT | GAAATTTTAA | ATTTAAACTA | ATGGAATCAA | 400 |
| GAAAGAATGA | AAGGAAATAT | ACAATGCCTA | CGATTAATAA | AAGGAAGTTT | 450 |
| ATTAGATTTT | GTGTTAGAAA | C | | | 471 |

2) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2082
- (C) ACCESSION NUMBER: AB013477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

| | | | | | |
|------------|------------|------------|-------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCACCAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACAG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2111
- (C) ACCESSION NUMBER: AB013478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACAG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 12

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/5495
- (C) ACCESSION NUMBER: AB013479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACAG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 13

- (i) (A) LENGTH: 478 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: 85/1836
 (C) ACCESSION NUMBER: AB013480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATCCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAAC | | | 478 |

2) INFORMATION FOR SEQ ID NO: 14.

- (i) (A) LENGTH: 479 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: 85/2147
 (C) ACCESSION NUMBER: AB013481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATCCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACA | | | 479 |

2) INFORMATION FOR SEQ ID NO: 15

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/3619
- (C) ACCESSION NUMBER: AB013482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCACCAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCNCGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |
| GAAGTTTATT | AGATTTTGTG | TTAGAAACAG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 16

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/3566
- (C) ACCESSION NUMBER: AB013483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCACCAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCGTATC | ATAAATAAAA | CTAAAAATTA | GGTTGTGTAT | AATTTAAAAA | 200 |
| TTTAATGAGA | TGTGGAGGAA | TTACATATAT | GAAATATTGG | ATTATACCTT | 250 |
| GCAATATCAT | ACGATGTTTA | TAGAGTGTTT | AATAAACCAT | TTTTCAACTA | 300 |
| TTGATGATCT | AGAATATATA | ATAACTGTAC | AAATTATATT | GATTATGGAA | 350 |
| CTACAATTAA | ATTAAGAAAT | TGATGATGAA | ATTTTAAATT | TAAACTAATG | 400 |
| GAATCAAGAA | AGAATGAAAG | GAAATATACA | ATGCCTACGA | TTAATAAAAG | 450 |

GAAGTTTATT AGATTTTGTG TTAGAACAG

480

2) INFORMATION FOR SEQ ID NO: 17

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2232
- (C) ACCESSION NUMBER: AB014402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

| | | | | | |
|------------|------------|-------------|-------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAAGTACGCA | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCATATC | ATAAATGATG | CGGTTTTTTC | AGCCGCTTCA | TAAAGGGATT | 200 |
| TTGAATGTAT | CAGAACATAT | GAGGTTTATG | TGAATTGCTG | TTATGTTTTT | 250 |
| AAGAAGCTTA | TCATAAGTAA | TGAGGTTTCAT | GATTTTTTGAC | ATAGTTAGCC | 300 |
| TCCGCAGTCT | TTCATTTCAA | GTAAATAATA | GCGAAATATT | CTTTATACTG | 350 |
| AATACTTATA | GTGAAGCAAA | GTTCTAGCTT | TGAGAAAATT | CTTTCTGCAA | 400 |
| CTAAATATAG | TAAATTACGG | TAAAATATAA | ATAAGTACAT | ATTGAAGAAA | 450 |
| ATGAGACATA | ATATATTTTA | TAATAGGAGG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 18

- (i) (A) LENGTH: 480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2235
- (C) ACCESSION NUMBER: AB014403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAAGTACGCA | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAGCAA | GTGTATAGAG | CATTTAAGAT | TATGCGTGGA | 150 |

| | | | | | |
|------------|------------|-------------|-------------|------------|-----|
| GAAGCATATC | ATAAATGATG | CGGTTTTTTC | AGCCGCTTCA | TAAAGGGATT | 200 |
| TTGAATGTAT | CAGAACATAT | GAGGTTTATG | TGAATTGCTG | TTATGTTTTT | 250 |
| AAGAAGCTTA | TCATAAGTAA | TGAGGTTTCAT | GATTTTTTGAC | ATAGTTAGCC | 300 |
| TCCGCAGTCT | TTCATTTCAA | GTAAATAATA | GCGAAATATT | CTTTATACTG | 350 |
| AATACTTATA | GTGAAGCAAA | GTTCTAGCTT | TGAGAAAATT | CTTTCTGCAA | 400 |
| CTAAATATAG | TAAATTACGG | TAAAATATAA | ATAAGTACAT | ATTGAAGAAA | 450 |
| ATGAGACATA | ATATATTTTA | TAATAGGAGG | | | 480 |

2) INFORMATION FOR SEQ ID NO: 19

- (i) (A) LENGTH: 458 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: MR108
- (C) ACCESSION NUMBER: AB014404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

| | | | | | |
|------------|------------|-------------|-------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCATATC | ATAAATGATG | CGGTTTTTTC | AGCCGCTTCA | TAAAGGGATT | 200 |
| TTGAATGTAT | CAGAACATAT | GAGGTTTATG | TGAATTGCTG | TTATGTTTTT | 250 |
| AAGAAGCTTA | TCATAAGTAA | TGAGGTTTCAT | GATTTTTTGAC | ATAGTTAGCC | 300 |
| TCCGCAGTCT | TTCATTTCAA | GTAAATAATA | GCGAAATATT | CTTTATACTG | 350 |
| AATACTTATA | GTGAAGCAAA | GTTCTAGCTT | TGAGAAAATT | CTTTCTGCAA | 400 |
| CTAAATATAG | TAAATTACGG | TAAAATATAA | ATAAGTACAT | ATTGAAGAAA | 450 |
| ATGAGACA | | | | | 458 |

2) INFORMATION FOR SEQ ID NO: 20

- (i) (A) LENGTH: 385 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/9302
- (C) ACCESSION NUMBER: AB014430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAGCAA | GTGTATAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCTTATC | ATAAGTAATG | AGGTTCATGA | TTTTTGACAT | AGTTAGCCTC | 200 |
| CGCAGTCTTT | CATTTCAAGT | AAATAATAGC | GAAATATTCT | TTATACTGAA | 250 |
| TACTTATAGT | GAAGCAAAGT | TCTAGCTTTG | AGAAAATTCT | TTCTGCAACT | 300 |
| AAATATAGTA | AATTACGGTA | AAATATAAAT | AAGTACATAT | TGAAGAAAAT | 350 |
| GAGACATAAT | ATATTTTATA | ATAGGAGGGA | ATTTC | | 385 |

2) INFORMATION FOR SEQ ID NO: 21

- (i) (A) LENGTH: 385 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: 84/9580
 (C) ACCESSION NUMBER: AB014431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAGCAA | GTGTATAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCTTATC | ATAAGTAATG | AGGTTCATGA | TTTTTGACAT | AGTTAGCCTC | 200 |
| CGCAGTCTTT | CATTTCAAGT | AAATAATAGC | GAAATATTCT | TTATACTGAA | 250 |
| TACTTATAGT | GAAGCAAAGT | TCTAGCTTTG | AGAAAATTCT | TTCTGCAACT | 300 |
| AAATATAGTA | AATTACGGTA | AAATATAAAT | AAGTACATAT | TGAAGAAAAT | 350 |
| GAGACATAAT | ATATTTTATA | ATAGGAGGGA | ATTTC | | 385 |

2) INFORMATION FOR SEQ ID NO: 22

- (i) (A) LENGTH: 385 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus

- (B) STRAIN: 85/1940
 (C) ACCESSION NUMBER: AB014432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAGCAA | GTGTATAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAAGCTTATC | ATAAGTAATG | AGGTTCATGA | TTTTTGACAT | AGTTAGCCTC | 200 |
| CGCAGTCTTT | CATTTCAAGT | AAATAATAGC | GAAATATTCT | TTATACTGAA | 250 |
| TACTTATAGT | GAAGCAAAGT | TCTAGCTTTG | AGAAAATTCT | TTCTGCAACT | 300 |
| AAATATAGTA | AATTACGGTA | AAATATAAAT | AAGTACATAT | TGAAGAAAAT | 350 |
| GAGACATAAT | ATATTTTATA | ATAGGAGGGA | ATTTC | | 385 |

2) INFORMATION FOR SEQ ID NO: 23

- (i) (A) LENGTH: 385 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: 61/6219
 (C) ACCESSION NUMBER: AB014433

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCG | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAAAG | CATTTAAGAT | TATGCGAGGA | 150 |
| GAAGCTTATC | ATAAGTAATG | AGGTTCATGA | TTTTTGACAT | AGTTAGCCTC | 200 |
| CGCAGTCTTT | CATTTCAAGT | AAATAATAGC | GAAATATTCT | TTATACTGAA | 250 |
| TACTTATAGT | GAAGCAAAGT | TCTAGCTTTG | AGAAAATTCT | TTCTGCAACT | 300 |
| AAATATAGTA | AATTACGGTA | AAATATAAAT | AAGTACATAT | TGAAGAAAAT | 350 |
| GAGACATAAT | ATATTTTATA | ATAGGAGGGA | ATTTC | | 385 |

2) INFORMATION FOR SEQ ID NO: 24

- (i) (A) LENGTH: 340 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: 64/4176
 (C) ACCESSION NUMBER: AB014434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CGCAGTAACT | ACGCGCTATC | ATTCAGCAAA | ATGACATTCC | CACATCAAAT | 50 |
| GATGCGGGTT | GTGTTAGTTG | AGCAAGTGTA | CATAGCATTT | AAGATTATGC | 100 |
| GAGGAGAAGC | TTATCATAAG | TAATGAGGTT | CATGATTTTT | GACATAGTTA | 150 |
| GCCTCCGCAG | TCTTTCATTT | CAAGTAAATA | ATAGCGAAAT | ATTCTTTATA | 200 |
| CTGAATACTT | ATAGTGAAGC | AAAGTTCTAG | CTTTGAGAAA | ATTCTTTCTG | 250 |
| CAACTAAATA | TAGTAAATTA | CGGTAAAATA | TAAATAAGTA | CATATTGAAG | 300 |
| AAAATGAGAC | ATAATATATT | TTATAATAGG | AGGGAATTTT | | 340 |

2) INFORMATION FOR SEQ ID NO: 25

- (i) (A) LENGTH: 369 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: 64/3846
 (C) ACCESSION NUMBER: AB014435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CAAACGGCCT | GCACAAGGAC | GTCTTACAAC | GCAGTAACTA | CGCACTATCA | 50 |
| TTCAGCAAAA | TGACATTCCC | ACATCAAATG | ATGCGGGTTG | TGTTAATTGA | 100 |
| ACAAGTGTAC | AGAGCATTTA | AGATTATGCG | AGGAGAAGCT | TATCATAAGT | 150 |
| AATGAGGTTT | ATGATTTTTG | ACATAGTTAG | CCTCCGCAGT | CTTTCATTTC | 200 |
| AAGTAAATAA | TAGCGAAATA | TTCTTTATAC | TGAATACTTA | TAGTGAAGCA | 250 |
| AAGTTCTAGC | TTTGAGAAAA | TTCTTTCTGC | AACTAAATAT | AGTAAATTAC | 300 |
| GGTAAATAT | AAATAAGTAC | ATATTGAAGA | AAATGAGACA | TAATATATTT | 350 |
| TATAATAGGA | GGGAATTTT | | | | 369 |

2) INFORMATION FOR SEQ ID NO: 26

- (i) (A) LENGTH: 3050 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: HUC19
 (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

| | | | | | |
|-------------|------------|------------|------------|------------|------|
| AATTTGGTAA | ACCTCAAAAG | GTAATTACAG | ATCAGGCACC | TTCAACGAAG | 50 |
| GTAGCAATGG | CTAAAGTAAT | TAAAGCTTTT | AAACTTAAAC | CTGACTGTCA | 100 |
| TTGTACATCG | AAATATCTGA | ATAACCTCAT | TGAGCAAGAT | CACCGTCATA | 150 |
| TTAAAGTAAG | AAAGACAAGG | TATCAAAGTA | TCAATACAGC | AAAGAATACT | 200 |
| TTAAAAGGTA | TTGAATGTAT | TCACGCTCTA | TATAAAAAGA | ACCGCAGGTC | 250 |
| TCTTCAGATC | TACGGATTTT | CGCCATGCCA | CGAAATTAGC | ATCATGCTAG | 300 |
| CAAGTTAAGC | GAACACTGAC | ATGATAAATT | AGTGGTTAGC | TATATTTTTT | 350 |
| TACTTTGCAA | CAGAACCGAA | AATAATCTCT | TCAATTTATT | TTTATATGAA | 400 |
| TCCTGTGACT | CAATGATTGT | AATATCTAAA | GATTTTCAGT | CATCATAGAC | 450 |
| AATGTTCTTT | TCAACATTTT | TTATAGCAAA | TTGATTAAAT | AAATTCTCTA | 500 |
| ATTTCTCCCG | TTTGATTTC | CTACCATAGA | TTATATTATC | ATTGATATAG | 550 |
| TCAATGAATA | ATGACAAATT | ATCACTCATA | ACAGTCCCAA | CCCCTTTATT | 600 |
| TTGATAGACT | AATTATCTTC | ATCATTTGTA | AACAAATTAC | ACCCTTTAAA | 650 |
| TTTAACTCAA | CTTAAATATC | GACAAATTAA | AAAACAATAA | AATTACTTGA | 700 |
| ATATTATTCA | TAATATATTA | ACAACCTTAT | TATACTGCTC | TTTATATATA | 750 |
| AAATCATTA | TAATTAAACA | AGCCTTAAAA | TATTTAACTT | TTTTGTGATT | 800 |
| ATTACACATT | ATCTTATCTG | CTCTTTATCA | CCATAAAAAT | AGAAAAACA | 850 |
| AGATTCCTAA | AGAATATAGG | AATCTTGTTT | CAGACTGTGG | ACAAACTGAT | 900 |
| TTTTTTATCAG | TTAGCTTATT | TAGAAAGTTT | TATTTAAATT | ACAGTTTCTA | 950 |
| TTTTTTATTAG | ATCACAATTT | TATTTTAGCT | CTTGTTCAAG | TAATCATTTT | 1000 |
| TCGCCAAAAA | CTTTATACTG | AATAGCTTCT | ACATTAAATA | CTTGTCAATG | 1050 |
| AGATCATCTA | CATCTTTAAA | TTCAGAATAA | TTCGCATATG | GATCTATAAA | 1100 |
| ATAAAATTGT | GGTTCTTTAC | CGGAAACATT | AAATATTCTT | AATATTAAAT | 1150 |
| ATTTCTGCTT | ATATTCTTTC | ATAGCAAACA | TTTCATTTAG | CGACATAAAA | 1200 |
| AATGGTTCCT | CAATACTAGA | AGATGTAGAT | GTTTTAATTT | CAATAAATTT | 1250 |
| TTCTACAGCT | TTATCTGTAT | TTGTTGGATC | AAAAGCTACT | AAATCATAGC | 1300 |
| CATGACCGTG | TTGAGAGCCT | GGATTATCAT | TTAAAATATT | CCTAAACTGT | 1350 |
| TCTTTCTTAT | CTTCGTCTAT | TTTATTATCA | ATTAGCTCAT | TAAAGTAATT | 1400 |
| TAGCGCTAAT | TTTTCTCCAA | CTTTACCGGT | TAATTTATTC | TCTTTATTTG | 1450 |
| ATTTTTCAAT | TTCTGAATCA | TTTTTAGTAG | TCTTTGATAC | ACCTTTTTTA | 1500 |
| TATTTTGGAA | TTATTCCTTT | AGGTGCTTCC | ACTTCCTTGA | GTGTCTTATC | 1550 |
| TTTTTGTGCT | GTTCTAATTT | CTTCAATTTT | GCTGTCTTCC | TGTATTTTCG | 1600 |
| CTATGCTATT | GACCAAGCTA | TCATAGGATG | TTTTTGTAAC | TTTTGAAGCT | 1650 |
| AATTCATTAA | ATAGTTCTAA | AAATTTCTTT | AAATCCTCTA | GCATATCTTC | 1700 |
| TTCTGTGAAT | CCTTCATTCA | AATCATAATA | TTTGAATCTT | ATTGATCCAT | 1750 |
| GAGAATATCC | TGATGGATAA | TCATTTTTTA | AATCATAAGA | TGAATCTTTA | 1800 |
| TTTTCTGCGT | AATAAAATCT | TCCAGTATTA | AATTCATTTG | ATGTAATATA | 1850 |
| TTTATTGAGT | TCGGAAGATA | AAGTTAATGC | TCTTTGTTTT | GCAGCATTTT | 1900 |
| TATCCCGCGG | AAACATATCA | CTTATCTTTG | ACCATCCTTG | ATTCAAAGAT | 1950 |
| AAGTATATGC | CTTCTCCTTC | CGGATGAAAA | AGATATACCA | AATAATGTCC | 2000 |
| ATCCTTTGTT | TCTTTTGTTA | TATTCTCATC | ATATATTGAA | ATCCAAGGAA | 2050 |
| CTTTACTATA | GTTCCAGTA | GCAACCTTCC | CTACAACTGA | ATATTTATCT | 2100 |
| TCTTTTATAT | GCACTTTTAA | CTGCTTGGGT | AACTTATCAT | GGACTAAAGT | 2150 |
| TTTATATAGA | TCACCTTTAT | CCCAATCAGA | TTTTTTAACT | ACATTATTGG | 2200 |

| | | | | | |
|-------------|------------|------------|------------|------------|------|
| TACGTTTCTC | TTTAATTAAT | TTAAGGACCT | GCATAAAGTT | GTCTATCATT | 2250 |
| TGAAATTCCC | TCCTATTATA | AAATATATTA | TGTCTCATTT | TCTTCAATAT | 2300 |
| GTAATTATTT | ATATTTTACC | GTAATTTACT | ATATTTAGTT | GCAGAAAGAA | 2350 |
| TTTTCTCAA | GCTAGAACTT | TGCTTCACTA | TAAGTATTCA | GTATAAAGAA | 2400 |
| TATTTGCTA | TTATTTACTT | GAAATGAAAG | ACTGCGGAGG | CTAACTATGT | 2450 |
| CAAAAATCAT | GAACCTCATT | ACTTATGATA | AGCTTCTTAA | AAACATAACA | 2500 |
| GCAATTCACA | TAAACCTCAT | ATGTTCTGAT | ACATTCAAAA | TCCCTTTATG | 2550 |
| AAGCGGCTGA | AAAAACCGCA | TCATTTATGA | TATGCTTCTC | CTCGCATAAT | 2600 |
| CTTAAATGCT | CTGTACACTT | GTTCAATTAA | CACAACCCGC | ATCATTTGAT | 2650 |
| GTGGGAATGT | CATTTTGCTG | AATGATAGTG | CGTAGTTACT | GCGTTGTAAG | 2700 |
| ACGTCCTTGT | GCAGGCCGTT | TGATCCGCCA | ATGACGAAAA | CAAAGTCGCT | 2750 |
| TTGCCCTTGG | GTCATGCGTT | GGTTCAATTC | TTGGGCCAAT | CCTTCGGAAG | 2800 |
| ATAGCATCTT | TCCTTGTATT | TCTAATGTAA | TGACTGTGGA | TTGTGGTTTG | 2850 |
| ATTTTGGCTA | GTATTCGTTG | GCCTTCTTTT | TCTTTTACTT | GCTCAATTTT | 2900 |
| TTTGTCACCTC | ATATTTTCTG | GTGCTTTTTT | GTCTGGAAC | TCTATGATGT | 2950 |
| CTATCTTGGT | GTATGGGCCT | AAACGTTTTT | CATATTCTGC | TATGGCTTGC | 3000 |
| TTCCAATATT | TCTCTTTTAG | TTTCCCTACA | GCTAAAATGG | TGATTTTCAT | 3050 |

2) INFORMATION FOR SEQ ID NO: 27

- (i) (A) LENGTH: 657 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CCACCTTCAT | ATGACGTCTA | TCCATTTATG | TATGGCATGA | GTAACGAAGA | 50 |
| ATATAATAAA | TTAACCGAAG | ATAAAAAAGA | ACCTCTGCTC | AACAAGTTCC | 100 |
| AGATTACAAC | TTCACCAGGT | TCAACTCAA | AAATATTAAC | AGCAATGATT | 150 |
| GGGTAAATA | ACAAAACATT | AGACGATAAA | ACAAGTTATA | AAATCGATGG | 200 |
| TAAAGGTTGG | CAAAAAGATA | AATCTTGGGG | TGGTTACAAC | GTTACAAGAT | 250 |
| ATGAAGTGGT | AAATGGTAAT | ATCGACTTAA | AACAAGCAAT | AGAATCATCA | 300 |
| GATAACATTT | TCTTTGCTAG | AGTAGCACTC | GAATTAGGCA | GTAAGAAATT | 350 |
| TGAAAAAGGC | ATGAAAAAAC | TAGGTGTTGG | TGAAGATATA | CCAAGTGATT | 400 |
| ATCCATTTTA | TAATGCTCAA | ATTTCAAACA | AAAATTTAGA | TAATGAAATA | 450 |
| TTATTAGCTG | ATTCAGGTTA | CGGACAAGGT | GAAATACTGA | TTAACCCAGT | 500 |
| ACAGATCCTT | TCAATCTATA | GCGCATTAGA | AAATAATGGC | AATATTAACG | 550 |
| CACCTCACTT | ATTAAAAGAC | ACGAAAAACA | AAGTTTGGAA | GAAAAATATT | 600 |
| ATTTCCAAAG | AAAATATCAA | TCTATTAACT | GATGGTATGC | AACAAGTCGT | 650 |
| AAATAAA | | | | | 657 |

2) INFORMATION FOR SEQ ID NO: 28

- (i) (A) LENGTH: 782 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: CCRI-1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CACCTTCATA | TGACGTCTAT | CCATTTATGT | ATGGCATGAG | TAACGAAGAA | 50 |
| TATAATAAAT | TAACCGAAGA | TAAAAAAGAA | CCTCTGCTCA | ACAAGTTCCA | 100 |
| GATTACAAC | TCACCAGGTT | CAACTCAAAA | AATATTAACA | GCAATGATTG | 150 |
| GGTTAAATAA | CAAAACATTA | GACGATAAAA | CAAGTTATAA | AATCGATGGT | 200 |
| AAAGGTTGGC | AAAAAGATAA | ATCTTGGGGT | GGTTACAACG | TTACAAGATA | 250 |
| TGAAGTGGTA | AATGGTAATA | TCGACTTAAA | ACAAGCAATA | GAATCATCAG | 300 |
| ATAACATTTT | CTTTGCTAGA | GTAGCACTCG | AATTAGGCAG | TAAGAAATTT | 350 |
| GAAAAAGGCA | TGAAAAAACT | AGGTGTTGGT | GAAGATATAC | CAAGTGATTA | 400 |
| TCCATTTTAT | AATGCTCAAA | TTTCAAACAA | AAATTTAGAT | AATGAAATAT | 450 |
| TATTAGCTGA | TTCAGGTTAC | GGACAAGGTG | AAATACTGAT | TAACCCAGTA | 500 |
| CAGATCCTTT | CAATCTATAG | CGCATTAGAA | AATAATGGCA | ATATTAACGC | 550 |
| ACCTCACTTA | TTAAAAGACA | CGAAAAACAA | AGTTTGGAAG | AAAAATATTA | 600 |
| TTTCCAAAGA | AAATATCAAT | CTATTAAC | ATGGTATGCA | ACAAGTCGTA | 650 |
| AATAAAACAC | ATAAAGAAGA | TATTTATAGA | TCTTATGCAA | ACTTAATTGG | 700 |
| CAAATCCGGT | ACTGCAGAAC | TCAAATGAA | ACAAGGAGAA | ACTGGCAGAC | 750 |
| AAATTGGGTG | GTTTATATCA | TATGATAAAG | AT | | 782 |

2) INFORMATION FOR SEQ ID NO: 29

- (i) (A) LENGTH: 744 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: CCRI-1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TATGACGTCT | ATCCATTAT | GTATGGCATG | AGTAACGAAG | AATATAATAA | 50 |
| ATTAACCGAA | GATAAAAAAG | AACCTCTGCT | CAACAAGTTC | CAGATTACAA | 100 |
| CTTCACCAGG | TTCAACTCAA | AAAATATTAA | CAGCAATGAT | TGGGTAAAT | 150 |
| AACAAAACAT | TAGACGATAA | AACAAGTTAT | AAAATCGATG | GTAAAGGTTG | 200 |
| GCAAAAAGAT | AAATCTTGGG | GTGGTTACAA | CGTTACAAGA | TATGAAGTGG | 250 |
| TAAATGGTAA | TATCGACTTA | AAACAAGCAA | TAGAATCATC | AGATAACATT | 300 |
| TTCTTTGCTA | GAGTAGCACT | CGAATTAGGC | AGTAAGAAAT | TTGAAAAAGG | 350 |
| CATGAAAAAA | CTAGGTGTTG | GTGAAGATAT | ACCAAGTGAT | TATCCATTTT | 400 |

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATAATGCTCA | AATTTCAAAC | AAAAATTTAG | ATAATGAAAT | ATTATTAGCT | 450 |
| GATTCAGGTT | ACGGACAAGG | TGAAATACTG | ATTAACCCAG | TACAGATCCT | 500 |
| TTCAATCTAT | AGCGCATTAG | AAAATAATGG | CAATATTAAC | GCACCTCACT | 550 |
| TATTAAAAGA | CACGAAAAAC | AAAGTTTGGA | AGAAAAATAT | TATTTCCAAA | 600 |
| GAAAATATCA | ATCTATTAAC | TGATGGTATG | CAACAAGTCG | TAAATAAAAC | 650 |
| ACATAAAGAA | GATATTTATA | GATCTTATGC | AAACTTAATT | GGCAAATCCG | 700 |
| GTAATGCAGA | ACTCAAAATG | AAACAAGGAG | AAACTGGCAG | ACAA | 744 |

2) INFORMATION FOR SEQ ID NO: 30

- (i) (A) LENGTH: 652 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CCACCTTCAT | ATGACGTCTA | TCCATTTATG | TATGGCATGA | GTAACGAAGA | 50 |
| ATATAATAAA | TTAACCGAAG | ATAAAAAAGA | ACCTCTGCTC | AACAAGTTCC | 100 |
| AGATTACAAC | TTCACCAGGT | TCAACTCAAA | AAATATTAAC | AGCAATGATT | 150 |
| GGGTTAAATA | ACAAAACATT | AGACGATAAA | ACAAGTTATA | AAATCGATGG | 200 |
| TAAAGGTTGG | CAAAAAGATA | AATCTTGGGG | TGGTTACAAC | GTTACAAGAT | 250 |
| ATGAAGTGGT | AAATGGTAAT | ATCGACTTAA | AACAAGCAAT | AGAATCATCA | 300 |
| GATAACATTT | TCTTTGCTAG | AGTAGCACTC | GAATTAGGCA | GTAAGAAATT | 350 |
| TGAAAAAGGC | ATGAAAAAAC | TAGGTGTTGG | TGAAGATATA | CCAAGTGATT | 400 |
| ATCCATTTTA | TAATGCTCAA | ATTTCAAACA | AAAATTTAGA | TAATGAAATA | 450 |
| TTATTAGCTG | ATTCAGGTTA | CGGACAAGGT | GAAATACTGA | TTAACCCAGT | 500 |
| ACAGATCCTT | TCAATCTATA | GCGCATTAGA | AAATAATGGC | AATATTAACG | 550 |
| CACCTCACTT | ATTAAAAGAC | ACGAAAAACA | AAGTTTGGAA | GAAAAATATT | 600 |
| ATTTCCAAAG | AAAATATCAA | TCTATTAACT | GATGGTATGC | AACAAGTCGT | 650 |
| AA | | | | | 652 |

2) INFORMATION FOR SEQ ID NO: 31

- (i) (A) LENGTH: 2436 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

| | | | | | |
|-------------|------------|-------------|-------------|------------|------|
| CCACCTTCAT | ATGACGTCTA | TCCATTTATG | TATGGCATGA | GTAACGAAGA | 50 |
| ATATAATAAA | TTAACCGAAG | ATAAAAAAGA | ACCTCTGCTC | AACAAGTTCC | 100 |
| AGATTACAAC | TTCACCAGGT | TCAACTCAAA | AAATATTAAC | AGCAATGATT | 150 |
| GGGTAAATA | ACAAAACATT | AGACGATAAA | ACAAGTTATA | AAATCGATGG | 200 |
| TAAAGGTTGG | CAAAAAGATA | AATCTTGGGG | TGGTTACAAC | GTTACAAGAT | 250 |
| ATGAAGTGGT | AAATGGTAAT | ATCGACTTAA | AACAAGCAAT | AGAATCATCA | 300 |
| GATAACATTT | TCTTTGCTAG | AGTAGCACTC | GAATTAGGCA | GTAAGAAATT | 350 |
| TGAAAAAGGC | ATGAAAAAAC | TAGGTGTTGG | TGAAGATATA | CCAAGTGATT | 400 |
| ATCCATTTTA | TAATGCTCAA | ATTTCAAACA | AAAATTTAGA | TAATGAAATA | 450 |
| TTATTAGCTG | ATTCAGGTTA | CGGACAAGGT | GAAATACTGA | TTAACCCAGT | 500 |
| ACAGATCCTT | TCAATCTATA | GCGCATTAGA | AAATAATGGC | AATATTAACG | 550 |
| CACCTCACTT | ATTAAAAGAC | ACGAAAAACA | AAGTTTGGAA | GAAAAATATT | 600 |
| ATTTCCAAAG | AAAATATCAA | TCTATTAACT | GATGGTATGC | AACAAGTCGT | 650 |
| AAATAAAACA | CATAAAGAAG | ATATTTATAG | ATCTTATGCA | AACTTAATTG | 700 |
| GCAAATCCGG | TACTGCAGAA | CTCAAAATGA | AACAAGGAGA | AACTGGCAGA | 750 |
| CAAATTGGGT | GGTTTATATC | ATATGATAAA | GATAATCCAA | ACATGATGAT | 800 |
| GGCTATTAAT | GTTAAAGATG | TACAAGATAA | AGGAATGGCT | AGCTACAATG | 850 |
| CCAAAATCTC | AGGTAAAGTG | TATGATGAGC | TATATGAGAA | CGGTAATAAA | 900 |
| AAATACGATA | TAGATGAATA | ACAAAACAGT | GAAGCAATCC | GTAACGATGG | 950 |
| TTGCTTCACT | GTTTTATTAT | GAATTATTAA | TAAGTGCTGT | TACTTCTCCC | 1000 |
| TTAAATACAA | TTTCTTCATT | TTCATTGTAT | GTTGAAAGTG | AACTGTAACT | 1050 |
| GAGTCCATTT | TCTTTTTTTA | TGGATTTCTT | ATTTGTAATT | TCAGCGATAA | 1100 |
| CGTACAATGT | ATTACCTGGG | TATACAGGTT | TAATAAATTT | AACGTTATTC | 1150 |
| ATTTGTGTTC | CTGCTACAAC | TTCTTCTCCG | TATTTACCTT | CTTCTACCCA | 1200 |
| TAATTTAAAT | GATATTGAAA | GTGTATGCAT | GCCAGATGCA | ATGATACCTT | 1250 |
| TAAATCTACT | TTGTTCTGCT | TTTTCTTTAT | CTATATGCAT | ATATTGAGGA | 1300 |
| TCAAAAGTTG | TTGCAAATTG | GATAATTTCT | TCTTCTGTAA | TATGAAGGCT | 1350 |
| TTTTGTTTTG | AATGTTTCTC | CTACTATAAA | ATCATCGTAT | TTCATATATG | 1400 |
| TCTCTCTTTC | TTATTCAAAT | TAATTTTTTTA | GTATGTAACA | TGTTAAAGGT | 1450 |
| AAGTCTACCG | TCACTGAAAC | GTAAGACTCA | CCTCTAACTT | TCTATTGAGA | 1500 |
| CAAATGCACC | ATTTTATCTG | CATTGTCTGT | AAAGATACCA | TCAACTCCCC | 1550 |
| AATTAGCAAG | TTGGTTTGCA | CGTGCTGGTT | TGTTTACAGT | CCATACGTTC | 1600 |
| AATTCATAAC | CCGCTTCTTT | TACCATTTTTT | ACTTTTGCTT | TAGTAAGTTT | 1650 |
| GGCATCTTCA | GTGTTTACTA | TTTTAGCATT | ACAGTAATCT | AAAAGTGTTT | 1700 |
| TCCAGTCTTC | ACGAAACGAA | GTTGTATGGA | ATATAACTGC | TCTGTTATAT | 1750 |
| TGTGGCATGA | TTTCTTCTGC | AAGTTTAAAC | AGCACAACAT | TAAAGCTTGA | 1800 |
| AATGAGCACT | TCTTGATTCT | GATTTAAGTT | TGTTAATTGT | TCTTCCACTT | 1850 |
| GCTTAACCAT | ACTTTTAGAA | AGTGCTAGTC | CATTCCGGTCC | AGTAATACCT | 1900 |
| TTTAATTCTA | CATTTAATTT | CATATTATAT | TCATTTGCTA | TTTTTACTAC | 1950 |
| ATCATCGAAA | GTTGGCAAAT | GTTTCATCTTT | GAATTTTTTCA | CCAAACCAAG | 2000 |
| ATCCTGCAGA | AGCATCTTTA | ATTTTCATCAT | AATTCAATTC | AGTTATTTCC | 2050 |
| CCGGACATAT | TTGTAGTCCG | TTCTAAATAA | TCATCATGAA | TGATAATCAG | 2100 |
| TTGTTTCATCT | TTTGTAATTG | CAACATCTAA | CTCCAACCAG | TTTATACCTT | 2150 |
| CTACTTCTGA | AGCAGCTTTA | AATGATGCAA | TTGTATTTTC | CGGAGCTTTA | 2200 |
| CTAGGTAATC | CTCTATGTCC | ATATACAGTT | AGCATATTAC | CTCTCCTTGC | 2250 |
| ATTTTTATTT | TTTTAATTAA | CGTAACTGTA | TTATCACATT | AATCGCACTT | 2300 |
| TTATTTCCAT | TAAAAAGAGA | TGAATATCAT | AAATAAAGAA | GTCGATAGAT | 2350 |
| TCGTATTGAT | TATGGAGTTA | ATCTACGTCT | CATCTCATTT | TTAAAAAATC | 2400 |
| ATTTATGTCC | CAAGCTCCAT | TTTGTAATCA | AGTCTA | | 2436 |

2) INFORMATION FOR SEQ ID NO: 32

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32

CGCTTGCCAC ATCAAATGAT GCGGGTTGTG CAAGCG

36

2) INFORMATION FOR SEQ ID NO: 33

- (i) (A) LENGTH: 336 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus epidermidis
- (B) STRAIN: G3
- (C) ACCESSION NUMBER: SEQ ID NO:15, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CTCATTACTT | ATGATAAGCT | TCTTAAAAAC | ATAACAGCAA | TTCACATAAA | 50 |
| CCTCATATGT | TCTGATACAT | TCAAATCCC | TTTATGAAGC | GGCTGAAAAA | 100 |
| ACCGCATCAT | TTATGATATG | CTTCGCCTCT | CATGATCTTA | AATGCGCGAT | 150 |
| AAATTTGTTC | GATCAATATG | ACGCGCATAT | TTGGTGTGGG | AAGGTCATAT | 200 |
| TGCTAAAAGA | TAAAGCATAG | TTGCTGCGTT | GTAAGACGTC | TTGGTGTAAG | 250 |
| CCATTGGAGC | CACCTATGAC | AAATGTAAAG | TCGCTTTGAC | CTTGTGTCAT | 300 |
| GCGTGTTTGT | AGTTCTTTAG | CGAGTCCTTC | TGAAGA | | 336 |

2) INFORMATION FOR SEQ ID NO: 34

- (i) (A) LENGTH: 260 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus haemolyticus
- (B) STRAIN: SH 518
- (C) ACCESSION NUMBER: SEQ ID NO:16, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CTCATTACTT | ATGATAAGCT | TCTTAAAAAC | ATAACAGCAA | TCCACATAAA | 50 |
| CCTCATATGT | TCTGATACAT | TCAAATCCC | TTTATGAAGC | GGCTGAAAAA | 100 |
| ACCGCATCAT | TTATGATATG | CTTCCCTCGC | ATGATTTTAA | ATGCTCTGTA | 150 |
| TACTTGCTCG | ATTAAGACAA | CGCGCATCAT | TTGATGTGGG | AATGTCATTT | 200 |
| TACTGAATGA | AAGTGCGTAG | TTGCTGCGTT | GTAAGACGTC | CTCATGCAAT | 250 |
| CCATTTGATC | | | | | 260 |

2) INFORMATION FOR SEQ ID NO: 35

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: ATCC 25923
- (C) ACCESSION NUMBER: SEQ ID NO:9, US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTTCA | GCAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAGGCGTATC | ACAAATAAAA | CTAAAAATGG | AGTAACTATT | AATATAGTAT | 200 |
| AAATTCAATA | TGGTGATAAA | AACAG | | | 225 |

2) INFORMATION FOR SEQ ID NO: 36

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: STP23
- (C) ACCESSION NUMBER: SEQ ID NO:10 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAGGCGTATC | ACAAATAAAA | CTAAAAATGG | AGTAACTATT | AATATAGTAT | 200 |
| AAATTCAATA | TGGTGATAAA | AACAG | | | 225 |

2) INFORMATION FOR SEQ ID NO: 37

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: STP43
- (C) ACCESSION NUMBER: SEQ ID NO:12 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGTAG | 50 |
| TAACTACGCA | CTATCATTCA | GCAAAATGAC | ATTTCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTACAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAGGCGTATC | ATAAGTAATG | AGGTTCATGA | TTTTTGACAT | AGTTAGCCTC | 200 |
| CGCAGTCTTT | CAAGTAAATA | ATATC | | | 225 |

2) INFORMATION FOR SEQ ID NO: 38

- (i) (A) LENGTH: 225 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: STP53
- (C) ACCESSION NUMBER: SEQ ID NO:13 US PATENT 6,156,507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTCGTCATTG | GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | 50 |
| TAACTACGCA | CTATCATTTA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | 100 |
| GGGTTGTGTT | AATTGAACAA | GTGTATAGAG | CATTTAAGAT | TATGCGTGGA | 150 |
| GAGGCGTATC | ATAAGTGATG | CTTGTTAGAA | TGATTTTAA | CAATATGAAA | 200 |

TAGCTGTGGA AGCTCAAACA TTTGT

225

2) INFORMATION FOR SEQ ID NO: 39

- (i) (A) LENGTH: 1500 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 476
- (C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

| | | | | | |
|------------|-------------|------------|------------|-------------|------|
| TGAGTCTGGT | AAAGATACAC | AACCAATTGG | TAAAGAGAAA | GTGATGAATC | 50 |
| CAGCGAAACA | ACCAGCGACA | GGTAAAGTTG | TGTTGTTACC | AGCGCATAGA | 100 |
| GGAAGTGTTA | GTAGCGGTAC | AGAAGGTTCT | GATCGCGCAT | TAGAAGGAAC | 150 |
| TGCTGTATCA | AGTAAGAGTG | GGAAACAATT | GGCTAACATG | TCAGCGCCTA | 200 |
| AAGGTAGCGC | ACATGAGAAA | CAGTTACCAA | AAACTGGAAC | TGATCAAAGT | 250 |
| TCAAGCCCAG | CAGCGATGTT | TGTATTAGTA | ACAGGTATAG | GTTTAATCGC | 300 |
| GACTGTACGA | CGTAGAAAAG | CTAGCTAAAA | TATATTGAAA | ACAATACTAC | 350 |
| TGTATTTCTT | AAATAAGAGG | TACGGTAGTG | TTTTTTTATG | GAAAAAAGCT | 400 |
| ATAACCGTTG | ATAAATATGG | GATATAAAAA | CGGGGATAAG | TAATAAGACA | 450 |
| TCAAGGTATT | TATCCACAGA | AATGGGGATA | GTTATCCAGA | ATTGTGTACA | 500 |
| ATTTAAAGAG | AAATACCCAC | AATGCCCACA | GAGTTATCCA | CAAATACACA | 550 |
| AGTTATACAC | TGAAAATTGG | GCATGAATGT | CAGAAAAATA | TCAAAAACCTG | 600 |
| CAAAAAAACT | TGGTATAATA | AGAGGGAAAA | GTGTGAACAA | GTTAATAACT | 650 |
| TGTGGATAAC | TGGAAAGTTG | ATAACAATTT | GGAGGACCAA | ACGACATGAA | 700 |
| AATCACCATT | TTAGcTGTAG | GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | 750 |
| CCATAGCAGA | ATATGAAAAA | CGTTTAGGCC | CATACACCAA | GATAGACATC | 800 |
| ATAGAAGTTA | CAGACGAAAA | AGCACCAGAA | AATATGAGCG | ACAAAGAAAT | 850 |
| CGAGCAAGTA | AAAGAAAAAG | AAGGCCAACG | AATACTAGCC | AAAATCAAAC | 900 |
| CACAATCCAC | AGTCATTACA | TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | 950 |
| GAAGGATTGG | CCCAAGAATT | GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | 1000 |
| CTTTGTATTG | GTCATTGGCG | GATCAAACGG | CCTGCACAAG | GACGTCTTAC | 1050 |
| AACGTAGTAA | CTACGCACTA | TCATTCAGCA | AAATGACATT | TCCACATCAA | 1100 |
| ATGATGCGGG | TTGTGTTAAT | TGAACAAGTG | TACAGAGCAT | TTAAGATTAT | 1150 |
| GCGTGGAGAA | GCTTATCATA | AATGATGCGG | TTTTTTCTTG | AAAAATTTAA | 1200 |
| TTAGATATTA | GAATCCTTTA | ATTTATTTGA | AAATCAGAAG | TGAGTAACAA | 1250 |
| TGGTAAGTGA | AATAGTTAGT | GCAATAATTG | GAATTATAGG | GATTTATTGA | 1300 |
| GATGTATGGA | GATGCGGGGC | ATTTATCGAG | TAGATTACAA | TTAGAGCATG | 1350 |
| TAGGTGATTT | GCTTTTTTCAT | GCAAGTAAAG | ATAAACTTTT | AAAAATCCTA | 1400 |
| TAAGAATTTA | GAAACTTTAG | AATAACTAAA | TATTAAAAAA | ATATCGTATG | 1450 |
| AAAGTGAAAT | TAGGATGAGA | GACCATAGCT | AAATTAAAAA | TTTTAGCAAA | 1500 |

2) INFORMATION FOR SEQ ID NO: 40

- (i) (A) LENGTH: 1501 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 252
- (C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

| | | | | | |
|-------------|-------------|------------|-------------|------------|------|
| TTGCACAACC | AATTGGTAAA | GACAAAGTGA | TGGATCCAGC | GAAACAACCA | 50 |
| GCGCCAAGTA | AAGTTGTATT | GTTGCCAGCG | CATAGAGGAA | CTGTTAGTAG | 100 |
| TGGTAGAGAA | GGTTC TGATC | GCGCATTGGA | AGGAACTGCT | GTATCAAGTA | 150 |
| AGAGCGGGAA | ACAATTGGCT | AGCATGTCAG | CGCCTAAAGG | TAGCACACAT | 200 |
| GAGAAGCAGT | TACCAAAAAC | TGGAAGTGAT | CAAAGTTCAA | GCCCAGCAGC | 250 |
| GATGTTTGTA | TTAGTAGCAG | GTATAGGTTT | AATTGCGACT | GTACGACGTA | 300 |
| GAAAAGCTAG | CTAAAATATA | TTGAAAACAA | TACTACTGTA | TTTCTTAAAC | 350 |
| AAGAGGTACG | GTAGTGTTTT | TTTATGAAAA | AAAGCTATAA | CCGTTGATAA | 400 |
| ATATGGGATA | TAAAAACGGG | GATAAGTAAT | AAGACATCAA | GGTATTTATC | 450 |
| CACAGAAATG | GGGATAGTTA | TCCAGAATTG | TGTACAATTT | AAAGAGAAAT | 500 |
| ACCCACAATG | CCCACAGAGT | TATCCACAAA | TACACAGGTT | ATACACTAAA | 550 |
| AATTGGGCGAT | GAATGTCAGA | AAAATATCAA | AAACTGCAAA | GAATATTGGT | 600 |
| ATAATAAGAG | GGAACAGTGT | GAACAAGTTA | ATAACTTG TG | GATAACTGGA | 650 |
| AAGTTGATAA | CAATTTGGAG | GACCAAACGA | CATGAAAATC | ACCATTTTAG | 700 |
| CTGTAGGGAA | ACTAAAAGAG | AAATATTGGA | AGCAAGCCAT | AGCAGAATAT | 750 |
| GAAAAACGTT | TAGGCCCAT A | CACCAAGATA | GACATCATAG | AAGTTCCAGA | 800 |
| CGAAAAAGCA | CCAGAAAATA | TGAGCGACAA | AGAAATTGAG | CAAGTAAAAG | 850 |
| AAAAAGAAGG | CCAACGAATA | CTAGCCAAAA | TCAAACCACA | ATCAACAGTC | 900 |
| ATTACATTAG | AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | GATTGGCCCA | 950 |
| AGAATTGAAC | CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | GTATTCGTCA | 1000 |
| TTGGCGGATC | AAACGGCCTG | CACAAGGACG | TCTTACAACG | CAGTAACTAC | 1050 |
| GCACTATCAT | TCAGCAAAAT | GACATTCCCA | CATCAAATGA | TGCGGGTTGT | 1100 |
| GTTAATTGAA | CAAGTGTACA | GAGCATTTAA | GATTATGCGT | GGAGAAGCAT | 1150 |
| ATCATAAATG | ATGCGGTTTT | TTCAGCCGCT | TCATAAAGGG | ATTTTGAATG | 1200 |
| TATCAGAACA | TATGAGGTTT | ATGTGAATTG | CTGTTATGTT | TTTAAGAAGC | 1250 |
| TTATCATAAG | TAATGAGGTT | CATGATTTTT | GACATAGTTA | GCCTCCGCAG | 1300 |
| TCTTTCATTT | CAAGTAAATA | ATAGCGAAAT | ATTCTTTATA | CTGAATACTT | 1350 |
| ATAGTGAAGC | AAAGTTCTAG | CTTTGAGAAA | ATTCTTTCTG | CAACTAAATA | 1400 |
| TAGTAAATTA | CGGTAAAATA | TAAATAAGTA | CATATTGAAG | AAAATGAGAC | 1450 |
| ATAATATATT | TTATAATAGG | AGGGAATTTT | AAATGATAGA | CAACTTTATG | 1500 |
| C | | | | | 1501 |

2) INFORMATION FOR SEQ ID NO: 41

- (i) (A) LENGTH: 2480 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: COL
- (C) ACCESSION NUMBER: Extracted from Genome project

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

| | | | | | |
|------------|-------------|------------|------------|-------------|------|
| AAACCGTCTG | GCAAACGAAT | TAATGCTATT | CAAATTTTAA | ATAAAGAGAC | 50 |
| AGGTAAGTTT | GAAAATATTG | ATTTAAAACG | TGTATATCAC | GTAACGATGA | 100 |
| ATGACTTCAC | AGCATCAGGT | GGCGACGGAT | ATAGTATGTT | CGGTGGTCCT | 150 |
| AGAGAAGAAG | GTATTTTCATT | AGATCAAGTA | CTAGCAAGTT | ATTTAAAAAC | 200 |
| AGCTAACTTA | GCTAAGTATG | ATACGACAGA | ACCACAACGT | ATGTTATTAG | 250 |
| GTAAACCAGC | AGTAAGTGAA | CAACCAGCTA | AAGGACAACA | AGGTAGCAAA | 300 |
| GGTAGTAAGT | CTGGTAAAGA | TACACAACCA | ATTGGTGACG | ACAAAGTGAT | 350 |
| GGATCCAGCG | AAAAAACCAG | CTCCAGGTAA | AGTTGTATTG | TTGCTAGCGC | 400 |
| ATAGAGGAAC | TGTTAGTAGC | GGTACAGAAG | GTTCTGGTCG | CACAATAGAA | 450 |
| GGAGCTACTG | TATCAAGCAA | GAGTGGGAAA | CAATTGGCTA | GAATGTCAGT | 500 |
| GCCTAAAGGT | AGCGCGCATG | AGAAACAGTT | ACCAAAAAC | GGAACATAATC | 550 |
| AAAGTTCAAG | CCCAGAAGCG | ATGTTTGTAT | TATTAGCAGG | TATAGGTTTA | 600 |
| ATCGCGACTG | TACGACGTAG | AAAAGCTAGC | TAAAATATAT | TGAAAATAAT | 650 |
| ACTACTGTAT | TTCTTAAATA | AGAGGTACGG | TAGTGTTTTT | TTATGAAAAA | 700 |
| AAGCGATAAC | CGTTGATAAA | TATGGGATAT | AAAAACGAGG | ATAAGTAATA | 750 |
| AGACATCAAG | GTGTTTATCC | ACAGAAATGG | GGATAGTTAT | CCAGAATTGT | 800 |
| GTACAATTTA | AAGAGAAATA | CCCACAATGC | CCACAGAGTT | ACCCACAAAT | 850 |
| ACACAGGTTA | TACACTAAAA | ATCGGGCATA | AATGTCAGGA | AAATATCAAA | 900 |
| AACTGCAAAA | AATATTGGTA | TAATAAGAGG | GAACAGTG | AACAAGTTAA | 950 |
| TAACTTGTGG | ATAACTGGAA | AGTTGATAAC | AATTTGGAGG | ACCAAACGAC | 1000 |
| ATGAAAATCA | CCATTTTAGC | TGTAGGGAAA | CTAAAAGAGA | AATATTGGAA | 1050 |
| GCAAGCCATA | GCAGAATATG | AAAAACGTTT | AGGCCCATAC | ACCAAGATAG | 1100 |
| ACATCATAGA | AGTTCCAGAC | GAAAAAGCAC | CAGAAAATAT | GAGTGACAAA | 1150 |
| GAAATTGAGC | AAGTAAAAGA | AAAAGAAGGC | CAACGAATAC | TAGCCAAAAT | 1200 |
| CAAACCACAA | TCCACAGTCA | TTACATTAGA | AATACAAGGA | AAGATGCTAT | 1250 |
| CTTCCGAAGG | ATTGGCCCAA | GAATTGAACC | AACGCATGAC | CCAAGGGCAA | 1300 |
| AGCGACTTTG | TTTTCGTCAT | TGGCGGATCA | AACGGCCTGC | ACAAGGACGT | 1350 |
| CTTACAACGC | AGTAACTACG | CACTATCATT | CAGCAAAATG | ACATTCCCAC | 1400 |
| ATCAAATGAT | GCGGGTTGTG | TTAATTGAAC | AAGTGACAG | AGCATTTAAG | 1450 |
| ATTATGCGAG | GAGAAGCTTA | TCATAAGTAA | TGAGGTTTAT | GATTTTTGAC | 1500 |
| ATAGTTAGCC | TCCGCAGTCT | TTCATTTCAA | GTAAATAATA | GCGAAATATT | 1550 |
| CTTTATACTG | AATACTTATA | GTGAAGCAAA | GTTCTAGCTT | TGAGAAAATT | 1600 |
| CTTTCTGCAA | CTAAATATAG | TAAATTACGG | TAAAATATAA | ATAAGTACAT | 1650 |
| ATTGAAGAAA | ATGAGACATA | ATATATTTTA | TAATAGGAGG | GAATTTCAAA | 1700 |
| TGATAGACAA | CTTTATGCAG | GTCCTTAAAT | TAATTAAAGA | GAAACGTACC | 1750 |
| AATAATGTAG | TTAAAAAATC | TGATTGGGAT | AAAGGTGATC | TATATAAAAC | 1800 |
| TTTAGTCCAT | GATAAGTTAC | CCAAGCAGTT | AAAAGTGCAT | ATAAAAGAAG | 1850 |

| | | | | | |
|------------|------------|------------|------------|------------|------|
| ATAAATATTC | AGTTGTAGGG | AAGGTTGCTA | CTGGGAACTA | TAGTAAAGTT | 1900 |
| CCTTGGATTT | CAATATATGA | TGAGAATATA | ACAAAAGAAA | CAAAGGATGG | 1950 |
| ATATTATTTG | GTATATCTTT | TTCATCCGGA | AGGAGAAGGC | ATATACTTAT | 2000 |
| CTTTGAATCA | AGGATGGTCA | AAGATAAGTG | ATATGTTTCC | GCGGGATAAA | 2050 |
| AATGCTGCAA | AACAAAGAGC | ATTAACCTTA | TCTTCCGAAC | TCAATAAATA | 2100 |
| TATTACATCA | AATGAATTTA | ATACTGGAAG | ATTTTATTAC | GCAGAAAATA | 2150 |
| AAGATTCATC | TTATGATTTA | AAAAATGATT | ATCCATCAGG | ATATTCTCAT | 2200 |
| GGATCAATAA | GATTCAAATA | TTATGATTTG | AATGAAGGAT | TCACAGAAGA | 2250 |
| AGATATGCTA | GAGGATTTAA | AGAAATTTTT | AGAACTATTT | AATGAATTAG | 2300 |
| CTTCAAAAGT | TACAAAAACA | TCCTATGATA | GCTTGGTCAA | TAGCATAGAC | 2350 |
| GAAATACAGG | AAGACAGCGA | AATTGAAGAA | ATTAGAACAG | CACAAAAAGA | 2400 |
| TAAGACACTC | AAGGAAGTGG | AAGCACCTAA | AGGAATAATT | CCAAAATATA | 2450 |
| AAAAGGTGT | ATCAAAGACT | ACTAAAAATG | | | 2480 |

2) INFORMATION FOR SEQ ID NO: 42

- (i) (A) LENGTH: 1045 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: ATCC 33592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

| | | | | | |
|------------|------------|------------|------------|------------|------|
| CCAGTTTTTT | GTTTAATGAA | CAAGGTAAAT | TACGAGATAA | TATTTGAAGA | 50 |
| AAACAATAAA | GTAGAGATGG | ATTTCCATAT | CCTCTTTAGT | AGCGGTTTTT | 100 |
| ATCTGTAAGG | TTTATTAATA | ATTAAATAAA | TAGGCGGGAT | AGTTATATAT | 150 |
| AGCTTATTAA | TGAAAGAATA | TGATTATTAA | TTTAGTATTA | TATTTTAATA | 200 |
| TTAAAAAGAA | GATATGAAAT | AATTATTCAT | ACCTTCCACC | TTACAATAAT | 250 |
| TAGTTTTTCA | TCGAATATTA | AGATTATTAG | TAGTCTTAAA | AGTTAAGACT | 300 |
| TCCTTATATT | AATGACCTAA | TTTATTATTT | GCCTCATGAA | TTATCTTTTT | 350 |
| ATTTCTTTGA | TATGTCCCAA | ACCACATCGT | GATATACACT | ACAATAAATA | 400 |
| TTATGATGAA | ACTAATAATA | TTCTCAAAGT | TCAGATGGAA | CCAACCTGCT | 450 |
| AGAATAGCGA | GTGGGAAGAA | TAGGATTATC | ATCAATATAA | AGTGAAGTAC | 500 |
| AGTCTGTTTT | GTTATACTCC | AATCGGTATC | TGTAAATATC | AAATTACCAT | 550 |
| AAGTAAACAA | AATTCCAATC | AATGCCCATA | GTGCTACACA | TATTAGCATA | 600 |
| ATAACCGCTT | CATTAAAGTT | TTCATAATAA | ATTTTACCCA | TAAAAGAATC | 650 |
| TGGATATAGT | GGTACATATT | TATCCCTTGA | AAAAAATAAG | TGAAGTAATG | 700 |
| ACAGAAATCA | TAAGACCAGT | GAACGCACCT | TTTTGAACAG | CGTGGAATAA | 750 |
| TTTTTTCATA | GTGAGATGGA | CCATTCCATT | TGTTTCTAAC | TTCAAGTGAT | 800 |
| CAATGTAATT | TAGATTGATA | ATTTCTGATT | TTGAAATACG | CACGAATATT | 850 |
| GAACCGACAA | GCTCTTCAAT | TTGGTAAAGT | CGCTGATAAA | GTTTTAAAGC | 900 |
| TTTATTATTC | ATTGTTATCG | CATACCTGTT | TATCTTCTAC | TATGAAGTGT | 950 |
| GCAATTTGTT | CTAGATCAAT | TGGGTAAACA | TGATGGTTCT | GTTGCAAAGT | 1000 |
| AAAAAAATAT | AGCTAACCAC | TAATTTATCA | TGTCAGTGTT | CGCTT | 1045 |

2) INFORMATION FOR SEQ ID NO: 43

- (i) (A) LENGTH: 1118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Staphylococcus aureus
 - (B) STRAIN: CCRI-8895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

| | | | | | | |
|------------|---|------------|------------|------------|------------|------|
| CAGAGCATT | T | AAGATTATGC | GTGGAGAAGC | GTACCACAAA | TGATGCGGTT | 50 |
| TTTTATCCAG | T | TTTTTTGTTT | AATGAACAAG | GTAAATTACG | AGATAATATT | 100 |
| TGAAGAAAAC | A | AATAAAGTAG | AGATGGATTT | CCATATCCTC | TTTAGTAGCG | 150 |
| GTTTTTATCT | G | TAAAGGTTTA | TTAATAATTA | AATAAATAGG | CGGGATAGTT | 200 |
| ATATATAGCT | T | ATTAATGAA | AGAATATGAT | TATTAATTTA | GTATTATATT | 250 |
| TTAATATTAA | A | AAGAAGATA | TGAAATAATT | ATTCATACCT | TCCACCTTAC | 300 |
| AATAATTAGT | T | TTCAATCGA | ATATTAAGAT | TATTAGTAGT | CTTAAAAGTT | 350 |
| AAGACTTCCT | T | ATATTAATG | ACCTAATTTA | TTATTTGCCT | CATGAATTAT | 400 |
| CTTTTTATTT | C | TTTGATATG | TCCCAAACCA | CATCGTGATA | TACACTACAA | 450 |
| TAAATATTAT | G | ATGAAACTA | ATAATATTCT | CAAAGTTCAG | ATGGAACCAA | 500 |
| CCTGCTAGAA | T | AGCGAGTGG | GAAGAATAGG | ATTATCATCA | ATATAAAGTG | 550 |
| AACATACAGT | C | TGTTTTGTTA | TACTCCAATC | GGTATCTGTA | AATATCAAAT | 600 |
| TACCATAAGT | A | AAACAAAATT | CCAATCAATG | CCCATAGTGC | TACACATATT | 650 |
| AGCATAATAA | C | CGCTTCATT | AAAGTTTTCA | TAATAAATTT | TACCCATAAA | 700 |
| AGAATCTGGA | T | ATAGTAGTA | CATATTTATC | CCTTGAAAAA | AATAAGTGAA | 750 |
| GTAATGACAG | A | AATCATAAG | ACCAGTGAAC | GCACCTTTTT | GAACAGCGTG | 800 |
| GAATAATTTT | T | TCATAGTGA | GATGGACCAT | TCCATTTGTT | TCTAACTTCA | 850 |
| AGTGATCAAT | G | TAATTTAGA | TTGATAATTT | CTGATTTTGA | AATACGCACG | 900 |
| AATATTGAAC | C | GACAAGCTC | TTCAATTTGG | TAAAGTCGCT | GATAAAGTTT | 950 |
| TAAAGCTTTA | T | TATTCATTG | TTATCGCATA | CCTGTTTATC | TTCTACTATG | 1000 |
| AACATGTCAA | T | TTGTTCTAG | ATCAATTGGG | TAAACATGAT | GGTTCTGTTG | 1050 |
| CAAAGTAAAA | A | ATATAGCT | AACCACTAAT | TTATCATGTC | AGTGTTGCTG | 1100 |
| TAACTTGCTA | G | CATGATG | | | | 1118 |

2) INFORMATION FOR SEQ ID NO: 44

- (i) (A) LENGTH: 1118 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear
- (ii) MOLECULE TYPE: Genomic DNA
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Staphylococcus aureus
 - (B) STRAIN: CCRI-8903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

| | | | | | | |
|------------|----|------------|------------|------------|------------|------|
| CAGAGCATT | TT | AAGATTATGC | GTGGAGAAGC | GTACCACAAA | TGATGCGGTT | 50 |
| TTTTATCCAG | | TTTTTTGTTT | AATGAACAAG | GTAAATTACG | AGATAATATT | 100 |
| TGAAGAAAAC | | AATAAAGTAG | AGATGGATTT | CCATATCCTC | TTTAGTAGCG | 150 |
| GTTTTTATCT | | GTAAGGTTTA | TTAATAATTA | AATAAATAGG | CGGGATAGTT | 200 |
| ATATATAGCT | | TATTAATGAA | AGAATATGAT | TATTAATTTA | GTATTATATT | 250 |
| TTAATATTAA | | AAAGAAGATA | TGAAATAATT | ATTCATACCT | TCCACCTTAC | 300 |
| AATAATTAGT | | TTTCAATCGA | ATATTAAGAT | TATTAGTAGT | CTTAAAAGTT | 350 |
| AAGACTTCCT | | TATATTAATG | ACCTAATTTA | TTATTTGCCT | CATGAATTAT | 400 |
| CTTTTTATTT | | CTTTGATATG | TCCCAAACCA | CATCGTGATA | TACACTACAA | 450 |
| TAAATATTAT | | GATGAAACTA | ATAATATTCT | CAAAGTTCAG | ATGGAACCAA | 500 |
| CCTGCTAGAA | | TAGCGAGTGG | GAAGAATAGG | ATTATCATCA | ATATAAAGTG | 550 |
| AACTACAGTC | | TGTTTTGTTA | TACTCCAATC | GGTATCTGTA | AATATCAAAT | 600 |
| TACCATAAGT | | AAACAAAATT | CCAATCAATG | CCCATAGTGC | TACACATATT | 650 |
| AGCATAATAA | | CCGCTTCATT | AAAGTTTTC | TAATAAATTT | TACCCATAAA | 700 |
| AGAATCTGGA | | TATAGTAGTA | CATATTTATC | CCTTGAAAAA | AATAAGTGAA | 750 |
| GTAATGACAG | | AAATCATAAG | ACCAGTGAAC | GCACCTTTTT | GAACAGCGTG | 800 |
| GAATAATTTT | | TTCATAGTGA | GATGGACCAT | TCCATTTGTT | TCTAACTTCA | 850 |
| AGTGATCAAT | | GTAATTTAGA | TTGATAATTT | CTGATTTTGA | AATACGCACG | 900 |
| AATATTGAAC | | CGACAAGCTC | TTCAATTTGG | TAAAGTCGCT | GATAAAGTTT | 950 |
| TAAAGCTTTA | | TTATTCATTG | TTATCGCATA | CCTGTTTATC | TTCTACTATG | 1000 |
| AACTGTGCAA | | TTTGTTCTAG | ATCAATTGGG | TAAACATGAT | GGTTCTGTTG | 1050 |
| CAAAGTAAAA | | AAATATAGCT | AACCACTAAT | TTATCATGTC | AGTGTTGCT | 1100 |
| TAACTTGCTA | | GCATGATG | | | | 1118 |

2) INFORMATION FOR SEQ ID NO: 45

- (i) (A) LENGTH: 1113 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-1324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| AGCATTTAAG | ATTATGCGTG | GAGAAGCGTA | CCACAAATGA | TGCGGTTTTT | 50 |
| TATCCAGTTT | TTTGTTTAAT | GAACAAGGTA | AATTACGAGA | TAATATTTGA | 100 |
| AGAAAACAAT | AAAGTAGAGA | TGGATTTCCA | TATCCTCTTT | AGTAGCGGTT | 150 |
| TTTATCTGTA | AGGTTTATTA | ATAATTAAAT | AAATAGGCGG | GATAGTTATA | 200 |
| TATAGCTTAT | TAATGAAAGA | ATATGATTAT | TAATTTAGTA | TTATATTTTA | 250 |
| ATATTAAAAA | GAAGATATGA | AATAATTATT | CATACCTTCC | ACCTTACAAT | 300 |
| AATTAGTTTT | CAATCGAATA | TTAAGATTAT | TAGTAGTCTT | AAAAGTTAAG | 350 |
| ACTTCCTTAT | ATTAATGACC | TAATTTATTA | TTTGCCTCAT | GAATTATCTT | 400 |
| TTTATTTCTT | TGATATGTCC | CAAACCACAT | CGTGATATAC | ACTACAATAA | 450 |
| ATATTATGAT | GAAACTAATA | ATATTCTCAA | AGTTCAGATG | GAACCAACCT | 500 |
| GCTAGAATAG | CGAGTGGGAA | GAATAGGATT | ATCATCAATA | TAAAGTGAAC | 550 |
| TACAGTCTGT | TTTGTTATAC | TCCAATCGGT | ATCTGTAAAT | ATCAAATTAC | 600 |
| CATAAGTAAA | CAAAATTCCA | ATCAATGCC | ATAGTGCTAC | ACATATTAGC | 650 |
| ATAATAACCG | CTTCATTAAA | GTTTTCATAA | TAAATTTTAC | CCATAAAAGA | 700 |
| ATCTGGATAT | AGTGGTACAT | ATTTATCCCT | TGAAAAAAT | AAGTGAAGTA | 750 |

| | | | | | |
|------------|------------|------------|-------------|------------|------|
| ATGACAGAAA | TCATAAGACC | AGTGAACGCA | CCTTTTTTGAA | CAGCGTGGAA | 800 |
| TAATTTTTC | ATAGTGAGAT | GGACCATTC | ATTTGTTTCT | AACTTCAAGT | 850 |
| GATCAATGTA | ATTTAGATTG | ATAATTTCTG | ATTTTGAAAT | ACGCACGAAT | 900 |
| ATTGAACCGA | CAAGCTCTTC | AATTTGGTAA | AGTCGCTGAT | AAAGTTTTAA | 950 |
| AGCTTTATTA | TTCATTGTTA | TCGCATACCT | GTTTATCTTC | TACTATGAAC | 1000 |
| TGTGCAATTT | GTTCTAGATC | AATTGGGTAA | ACATGATGGT | TCTGTTGCAA | 1050 |
| AGTAAAAAAA | TATAGCTAAC | CACTAATTTA | TCATGTCAGT | GTTCGCTTAA | 1100 |
| CTTGCTAGCA | TGA | | | | 1113 |

2) INFORMATION FOR SEQ ID NO: 46

- (i) (A) LENGTH: 2153 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double.
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

| | | | | | |
|------------|--------------|------------|------------|-------------|------|
| CTGTAGGGAA | ACTAAAAGAG | AAATACTGGA | AGCAAGCCAT | AGCAGAATAT | 50 |
| GAAAAACGTT | TAGGCCCATATA | CACCAAGATA | GACATCATAG | AAGTTCCAGA | 100 |
| CGAAAAAGCA | CCAGAAAATA | TGAGCGACAA | AGAAATCGAG | CAAGTAAAAG | 150 |
| AAAAAGAAGG | CCAACGAATA | CTAGCCAAAA | TCAAACCACA | ATCCACAGTC | 200 |
| ATTACATTAG | AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | GATTGGCCCA | 250 |
| AGAATTGAAC | CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | GTATTTCGTCA | 300 |
| TTGGCGGATC | AAACGGCCTG | CACAAGGACG | TCTTACAACG | CAGTAACTAC | 350 |
| GCACTATCAT | TCAGCAAAAT | GACATTCCCA | CATCAAATGA | TGCGGGTTGT | 400 |
| GTTAATTGAA | CAAGTGTACA | GAGCATTTAA | GATTATGCGT | GGAGAAGCGT | 450 |
| ACCACAAATG | ATGCGGTTTT | TTATCCAGTT | TTTTGTTTAA | TGAACAAGGT | 500 |
| AAATTACGAG | ATAATATTTG | AAGAAAACAA | TAAAGTAGAG | ATGGATTTC | 550 |
| ATATCCTCTT | TAGTAGCGGT | TTTTATCTGT | AAGGTTTATT | AATAATTAAA | 600 |
| TAAATAGGCG | GGATAGTTAT | ATATAGCTTA | TTAATGAAAG | AATATGATTA | 650 |
| TTAATTTAGT | ATTATATTTT | AATATTAAAA | AGAAGATATG | AAATAATTAT | 700 |
| TCATACCTTC | CACCTTACAA | TAATTAGTTT | TCAATCGAAT | ATTAAGATTA | 750 |
| TTAGTAGTCT | TAAAAGTTAA | GACTTCCTTA | TATTAATGAC | CTAATTTATT | 800 |
| ATTTGCCTCA | TGAATTATCT | TTTTATTTCT | TTGATATGTC | CCAAACCACA | 850 |
| TCGTGATATA | CACTACAATA | AATATTATGA | TGAAACTAAT | AATATTCTCA | 900 |
| AAGTTCAGAT | GGAACCAACC | TGCTAGAATA | GCGAGTGGGA | AGAATAGGAT | 950 |
| TATCATCAAT | ATAAAGTGAA | CTACAGTCTG | TTTTGTTATA | CTCCAATCGG | 1000 |
| TATCTGTAAA | TATCAAATTA | CCATAAGTAA | ACAAAATTCC | AATCAATGCC | 1050 |
| CATAGTGCTA | CACATATTAG | CATAATAACC | GCTTCATTAA | AGTTTTCATA | 1100 |
| ATAAATTTTA | CCCATAAAAG | AATCTGGATA | TAGTGGTACA | TATTTATCCC | 1150 |
| TTGAAAAAAA | TAAGTGAAGT | AATGACAGAA | ATCATAAGAC | CAGTGAACGC | 1200 |
| ACCTTTTTGA | ACAGCGTGGA | ATAATTTTTT | CATAGTGAGA | TGGACCATTC | 1250 |
| CATTTGTTTC | TAACTTCAAG | TGATCAATGT | AATTTAGATT | GATAATTTCT | 1300 |
| GATTTTGAAA | TACGCACGAA | TATTGAACCG | ACAAGCTCTT | CAATTTGGTA | 1350 |
| AAGTCGCTGA | TAAAGTTTAA | AAGCTTTATT | ATTCATTGTT | ATCGCATACC | 1400 |
| TGTTTATCTT | CTACTATGAA | CTGTGCAATT | TGTTCTAGAT | CAATTGGGTA | 1450 |
| AACATGATGG | TTCTGTTGCA | AAGTAAAAAA | ATATAGCTAA | CCACTAATTT | 1500 |
| ATCATGTCAG | TGTTTCGCTTA | ACTTGCTAGC | ATGATGCTAA | TTTCGTGGCA | 1550 |

| | | | | | |
|------------|-------------|------------|------------|-------------|------|
| TGGCGAAAAT | CCGTAGATCT | GATGAGACCT | GCGGTTCTTT | TTATATAGAG | 1600 |
| CGTAAATACA | TTCAATACCT | TTTAAAGTAT | TCTTTGCTGT | ATTGATACTT | 1650 |
| TGATACCTTG | TCTTTCTTAC | TTTAATATGA | CGGTGATCTT | GCTCAATGAG | 1700 |
| GTTATTCAAA | TATTTTCGATG | TACAATGACA | GTCAGGTTTA | AGTTTAAAAG | 1750 |
| CTTTAATTAC | TTTAGCCATT | GCTACCTTCG | TTGAAGGTGC | CTGATCTGTA | 1800 |
| ATTACCTTTT | GAGGTTTACC | AAATTGTTTA | ATGAGACGTT | TAATAAACGC | 1850 |
| ATATGCTGAA | TGATTATCTC | GTTGCTTACG | CAACCAAATA | TCTAATGTAT | 1900 |
| GTCCTCTGTC | ATCAATGGCA | CGATATAAAT | AGCTCCATTT | TCCTTTTATT | 1950 |
| TTGATGTACG | TCTCATCAAT | ACGCCATTTG | TAATAAGCTT | TTTTATGCTT | 2000 |
| TTTCTTCCAA | ATTTGATATA | AAATTGGGGC | ATATTCTTGA | ACCCAACGGT | 2050 |
| AGACCGTTGA | ATGATGAACG | TTTACACCAC | GTCCCCTTAA | TATTTTCAGAT | 2100 |
| ATATCACGAT | AACTCAATGC | ATATCTTAGA | TAGTAGCCAA | CGGCTACAGT | 2150 |
| GAT | | | | | 2153 |

2) INFORMATION FOR SEQ ID NO: 47

- (i) (A) LENGTH: 737 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (B) STRAIN: CCRI-1263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

| | | | | | |
|------------|-------------|------------|------------|-------------|-----|
| TTTAAGATTA | TGCGTGGAGA | AGCATATCAT | AAATGATGCG | GTTATTTTCAG | 50 |
| CCGTAATTTT | ATAATATAAA | GCAGAGTTTA | TTAAATTTTA | ATGATTACTT | 100 |
| TTTATTAAGA | ATTAATTCTA | GTTGATATAT | TATAATGTGA | AACACAAAAT | 150 |
| AATAATTTGT | AATTGTTAGT | TTATAGGCAT | CTGTATTTGG | AATTTTTTGT | 200 |
| AGACTATTTA | AAAAATAGTG | TATATAAGTA | TTGAGTTCAT | GTATTAAGTG | 250 |
| TCTTTTTTCA | TCGTTTCATCA | AGTATAAGGA | TGTAGAGATT | TGTTGGATAA | 300 |
| TTTCTTCGGA | TGTTTTTAAA | ATTATCATTA | AATTAGATGG | TATCTGATCT | 350 |
| TGAGTTTTGT | TTTTAGTGTA | TGTATATTTT | AAAAAATTTT | TGATTGTTGT | 400 |
| TATTTGACTC | TCTTTTAAAT | TGACACCCTC | ATCAATAAAT | GTGTTAAATA | 450 |
| TATCTTCATT | TGTACTTAAA | TCATCAAAAT | TTGCCAACAA | ATATTTGAAC | 500 |
| GTCTCTAAAT | CATTATGTTT | GAGTTCGGTT | TTGCTATTCC | ATAATTCCAA | 550 |
| ACCATTTGGT | AGAAAGCCCA | AGCTGTGATT | TTGATCTCCC | CATATAGCTG | 600 |
| AATTTAAATC | AGTGAGTTGA | TTAATTTTTT | CAACACAGAA | ATGTAATTTT | 650 |
| GGAATGAGGA | ATCGAAGTTG | TTCTTCTACT | TGCTGTACTT | TTCTTTTGTT | 700 |
| TTCAATAAAA | TTTCTACACC | ATACTGTTAT | CAAACCG | | 737 |

2) INFORMATION FOR SEQ ID NO: 48

- (i) (A) LENGTH: 1592 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

| | | | | | |
|-------------|------------|-------------|------------|------------|------|
| AACTAAAAGA | GAAATATTGG | AAGCAAGCCA | TAGCAGAATA | TGAAAAACGT | 50 |
| TTAGGCCCAT | ACACCAAGAT | AGACATCATA | GAAGTTCCAG | ACGAAAAAGC | 100 |
| ACCAGAAAAT | ATGAGTGACA | AAGAAATTGA | GCAAGTAAAA | GAAAAAGAAG | 150 |
| GCCAACGAAT | ACTAGCCAAA | ATCAAACCAC | AATCCACAGT | CATTACATTA | 200 |
| GAAATACAAG | GAAAGATGCT | ATCTTCCGAA | GGATTGGCCC | AAGAATTGAA | 250 |
| CCAACGCATG | ACCCAAGGGC | AAAGCGACTT | TGTTTTCGTC | ATTGGCGGAT | 300 |
| CAAACGGCCT | GCACAAGGAC | GTCTTACAAC | GCAGTAACTA | CGCACTATCA | 350 |
| TTCAGCAAAA | TGACATTCCC | ACATCAAATG | ATGCGGGTTG | TGTTAATTGA | 400 |
| ACAAGTGTAC | AGAGCATTTA | AGATTATGCG | AGGAGAAGCA | TATCATAAAT | 450 |
| GATGCGGTTA | TTTCAGCCGT | AATTTTATAA | TATAAAGCAG | AGTTTATTAA | 500 |
| ATTTTAATGA | TTACTTTTTA | TTAAGAATTA | ATTCTAGTTG | ATATATTATA | 550 |
| ATGTGAAACA | CAAAATAATA | ATTTGTAATT | GTTAGTTTAT | AGGCATCTGT | 600 |
| ATTTGGAATT | TTTTGTAGAC | TATTTAAAAA | ATAGTGTATA | TAAGTATTGA | 650 |
| G TTCATGTAT | TAACTGTCTT | TTTTTCATCGT | TCATCAAGTA | TAAGGATGTA | 700 |
| GAGATTTGTT | GGATAATTTC | TTCGGATGTT | TTTAAAATTA | TCATTAAATT | 750 |
| AGATGGTATC | TGATCTTGAG | TTTTGTTTTT | AGTGTATGTA | TATTTTAAAA | 800 |
| AATTTTGTGAT | TGTTGTTATT | TGACTCTCTT | TTAATTTGAC | ACCCTCATCA | 850 |
| ATAAATGTGT | TAAATATATC | TTCATTTGTA | CTTAAATCAT | CAAAATTTGC | 900 |
| CAACAAATAT | TTGAACGTCT | CTAAATCATT | ATGTTTGAGT | TCCGTTTTGC | 950 |
| TATTCCATAA | TTCCAAACCA | TTTGGTAGAA | AGCCCAAGCT | GTGATTTTGA | 1000 |
| TCTCCCCATA | TAGCTGAATT | TAAATCAGTG | AGTTGATTAA | TTTTTTCAAC | 1050 |
| ACAGAAATGT | AATTTTGGAA | TGAGGAATCG | AAGTTGTTCT | TCTACTTGCT | 1100 |
| GTACTTTTCT | TTTGTTTTCA | ATAAAATTTC | TACACCATAC | TGTTATCAAA | 1150 |
| CCGCCAATTA | TTGTGCACAA | TCCTCCAATG | ATTGTAGATA | AAATTGACAA | 1200 |
| TATATTACAC | ACCTTTCTTA | GAGGTTTATT | AACATCTATT | TTTGAATTTA | 1250 |
| AAATTATTAC | TTTGGTAGCG | TTATAACCTA | TTTAACAGAT | TAGAGAAAAA | 1300 |
| TTGAATGATC | GATTGAAGAA | TTTCCAAAAT | ACCGTCCCAT | ATGCGTTGAA | 1350 |
| GGAGATTTCT | ATTTTCTTCT | GTATTCAAAT | CTTTGGCTTT | ATCCTTTGCT | 1400 |
| TTATTCAATA | AATCATCTGA | GTTTTTTTCA | ATATTTTTTA | ATACATCTTT | 1450 |
| GGCATTTTGT | TTAAATACTT | TAGGATCGGA | AGTTAGGGCA | TTAGAGTTTG | 1500 |
| CCACATTAAT | CATATTATTA | TTAATCATTT | GAATTTGATT | ATCTGATAAT | 1550 |
| ATCTCTGATA | ACCTACGCTC | ATCGAGGACT | TTATTAACAG | TG | 1592 |

2) INFORMATION FOR SEQ ID NO: 49

- (i) (A) LENGTH: 730 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
(B) STRAIN: CCRI-1311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

| | | | | | |
|-------------|-------------|------------|------------|------------|-----|
| AGCATTTAAG | ATTATGCGTG | GAGAAGCATA | TCATAAATGA | TGCGGTTATT | 50 |
| TCAGCCGTAA | TTTTATAATA | TAAAGCAGAG | TTTATTAAAT | TTTAATGATT | 100 |
| ACTTTTTTATT | AAGAATTAAT | TCTAGTTGAT | ATATTATAAT | GTGAAACACA | 150 |
| AAATAATAAT | TTGTAATTGT | TAGTTTATAG | GCATCTGTAT | TTGGAATTTT | 200 |
| TTGTAGACTA | TTTAAAAAAT | AGTGTATATA | AGTATTGAGT | TCATGTATTA | 250 |
| ACTGTCTTTT | TTCATCGTTC | ATCAAGTATA | AGGATGTAGA | GATTTGTTGG | 300 |
| ATAATTTCTT | CGGATGTTTT | TAAAATTATC | ATTAAATTAG | ATGGTATCTG | 350 |
| ATCTTGAGTT | TTGTTTTTTAG | TGTATGTATA | TTTTAAAAAA | TTTTTGATTG | 400 |
| TTGTTATTTG | ACTCTCTTTT | AATTTGACAC | CCTCATCAAT | AAATGTGTTA | 450 |
| AATATATCTT | CATTTGTACT | TAAATCATCA | AAATTTGCCA | ACAAATATTT | 500 |
| GAACGTCTCT | AAATCATTAT | GTTTGAGTTC | CGTTTTGCTA | TTCCATAATT | 550 |
| CCAAACCATT | TGGTAGAAAG | CCCAAGCTGT | GATTTTGATC | TCCCCATATA | 600 |
| GCTGAATTTA | AATCAGTGAG | TTGATTAATT | TTTTCAACAC | AGAAATGTAA | 650 |
| TTTTGGAATG | AGGAATCGAA | GTTGTTCTTC | TACTTGCTGT | ACTTTTCTTT | 700 |
| TGTTTTCAAT | AAAATTTCTA | CACCATACTG | | | 730 |

2) INFORMATION FOR SEQ ID NO: 50

- (i) (A) LENGTH: 1696 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

| | | | | | |
|------------|------------|------------|------------|------------|------|
| AAAGAGAAAT | ATTGGAAGCA | AGCCATAGCA | GAATATGAAA | AACGTTTAGG | 50 |
| CCCATACACC | AAGATAGACA | TCATAGAAGT | TCCAGACGAA | AAAGCACCAG | 100 |
| AAAATATGAG | TGACAAAGAA | ATTGAGCAAG | TAAAAGAAAA | AGAAGGCCAA | 150 |
| CGAATACTAG | CCAAAATCAA | ACCACAATCC | ACAGTCATTA | CATTAGAAAT | 200 |
| ACAAGGAAAG | ATGCTATCTT | CCGAAGGATT | GGCCCAAGAA | TTGAACCAAC | 250 |
| GCATGACCCA | AGGGCAAAGC | GACTTTGTTT | TCGTCAATTG | CGGATCAAAC | 300 |
| GGCCTGCACA | AGGACGTCTT | ACAACGCAGT | AACACGCAC | TATCATTCAG | 350 |
| CAAAATGACA | TTCCCACATC | AAATGATGCG | GGTTGTGTTA | ATTGAACAAG | 400 |
| TGTACAGAGC | ATTTAAGATT | ATGCGAGGAG | AAGCATATCA | TAAATGATGC | 450 |
| GGTTATTTCA | GCCGTAATTT | TATAATATAA | AGCAGAGTTT | ATTAAATTTT | 500 |
| AATGATTACT | TTTTATTAAG | AATTAATTCT | AGTTGATATA | TTATAATGTG | 550 |
| AAACACAAAA | TAATAATTTG | TAATTGTTAG | TTTATAGGCA | TCTGTATTTG | 600 |
| GAATTTTTTG | TAGACTATTT | AAAAAATAGT | GTATATAAGT | ATTGAGTTCA | 650 |
| TGTATTAACT | GTCTTTTFTC | ATCGTTCATC | AAGTATAAGG | ATGTAGAGAT | 700 |
| TTGTTGGATA | ATTTCTTCGG | ATGTTTTTAA | AATTATCATT | AAATTAGATG | 750 |
| GTATCTGATC | TTGAGTTTTG | TTTTTAGTGT | ATGTATATTT | TAAAAAATTT | 800 |
| TTGATTGTTG | TTATTTGACT | CTCTTTTAA | TTGACACCCT | CATCAATAAA | 850 |
| TGTGTTAAAT | ATATCTTCAT | TTGTACTTAA | ATCATCAAAA | TTTGCCAACA | 900 |
| AATATTTGAA | CGTCTCTAAA | TCATTATGTT | TGAGTTCCGT | TTTGCTATTC | 950 |
| CATAATTCCA | AACCATTTGG | TAGAAAGCCC | AAGCTGTGAT | TTTGATCTCC | 1000 |
| CCATATAGCT | GAATTTAAAT | CAGTGAGTTG | ATTAATTTTT | TCAACACAGA | 1050 |
| AATGTAATTT | TGGAATGAGG | AATCGAAGTT | GTTCTTCTAC | TTGCTGTACT | 1100 |

| | | | | | |
|------------|------------|------------|------------|------------|------|
| TTTCTTTTGT | TTTCAATAAA | ATTTCTACAC | CATACTGTTA | TCAAACCGCC | 1150 |
| AATTATTGTG | CACAATCCTC | CAATGATTGT | AGATAAAATT | GACAATATAT | 1200 |
| TACACACCTT | TCTTAGAGGT | TTATTAACAT | CTATTTTGA | ATTTAAAATT | 1250 |
| ATTACTTTGG | TAGCGTTATA | ACCTATTTAA | CAGATTAGAG | AAAAATTGAA | 1300 |
| TGATCGATTG | AAGAATTTCC | AAAATACCGT | CCCATATGCG | TTGAAGGAGA | 1350 |
| TTTCTATTTT | CTTCTGTATT | CAAATCTTTG | GCTTTATCCT | TTGCTTTATT | 1400 |
| CAATAAATCA | TCTGAGTTTT | TTTCAATATT | TTTTAATACA | TCTTTGGCAT | 1450 |
| TTTGTTTAAA | TACTTTAGGA | TCGGAAGTTA | GGGCATTAGA | GTTTGCCACA | 1500 |
| TTAATCATAT | TATTATTAAT | CATTTGAATT | TGATTATCTG | ATAATATCTC | 1550 |
| TGATAACCTA | CGCTCATCGA | GGACTTTATT | AACAGTGTCT | TCAACTTGTT | 1600 |
| GTTGTGTGAT | TTGTTTATCT | TGATTTTGTG | TAATATCTGC | AAGTTGTTCT | 1650 |
| TTAATATCTG | CTATAGAAGC | ATTTAAAGCT | TCATCTGAAT | ACCCAT | 1696 |

2) INFORMATION FOR SEQ ID NO: 51

- (i) (A) LENGTH: 2122 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

| | | | | | |
|------------|-------------|-------------|-------------|------------|------|
| GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | CCATAGCAGA | ATATGAAAAA | 50 |
| CGTTTAGGCC | CATACACCAA | GATAGACATC | ATAGAAGTTC | CAGACGAAAA | 100 |
| AGCACCAGAA | AATATGAGCG | ACAAAGAAAT | TGAGCAAGTA | AAAGAAAAAG | 150 |
| AAGGCCAACG | AATACTAGCC | AAAATCAAAC | CACAATCAAC | AGTCATTACA | 200 |
| TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | GAAGGATTGG | CCCAAGAATT | 250 |
| GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | CTTTGTATTTC | GTCATTGGCG | 300 |
| GATCAAACGG | CCTGCACAAG | GACGTCTTAC | AACGCAGTAA | CTACGCACTA | 350 |
| TCATTCAGCA | AAATGACATT | CCCACATCAA | ATGATGCGGG | TTGTGTTAAT | 400 |
| TGAACAAGTG | TACAGAGCAT | TTAAGATTAT | GCGTGGAGAA | GCGTACCACA | 450 |
| AATGATGCGG | TTTTTTTATCC | AGTTTTTTTGT | TTAATGAACA | AGGTAAATTA | 500 |
| CGAGATAATA | TTTGAAGAAA | ACAATAAAGT | AGAGATGGAT | TTCCATATCC | 550 |
| TCTTTAGTAG | CGGTTTTTTAT | CTGTAAGGTT | TATTAATAAT | TAAATAAATA | 600 |
| GGCGGGATAG | TTATATATAG | CTTATTAATG | AAAGAATATG | ATTATTAATT | 650 |
| TAGTATTATA | TTTTAATATT | AAAAAGAAGA | TATGAAATAA | TTATTCATAC | 700 |
| CTTCCACCTT | ACAATAATTA | GTTTTCAATC | GAATATTAAG | ATTATTAGTA | 750 |
| GTCTTAAAAG | TTAAGACTTC | CTTATATTAA | TGACCTAATT | TATTATTTGC | 800 |
| CTCATGAATT | ATCTTTTTTAT | TTCTTTGATA | TGTCCCAAAC | CACATCGTGA | 850 |
| TATACACTAC | AATAAATATT | ATGATGAAAC | TAATAATATT | CTCAAAGTTC | 900 |
| AGATGGAACC | AACCTGCTAG | AATAGCGAGT | GGGAAGAATA | GGATTATCAT | 950 |
| CAATATAAAG | TGAACTACAG | TCTGTTTTTGT | TATACTCCAA | TCGGTATCTG | 1000 |
| TAAATATCAA | ATTACCATAA | GTAAACAAAA | TTCCAATCAA | TGCCCATAGT | 1050 |
| GCTACACATA | TTAGCATAAT | AACCGCTTCA | TTAAAGTTTT | CATAATAAAT | 1100 |
| TTTACCCATA | AAAGAATCTG | GATATAGTGG | TACATATTTA | TCCCTTGAAA | 1150 |
| AAAATAAGTG | AAGTAATGAC | AGAAATCATA | AGACCAGTGA | ACGCACCTTT | 1200 |
| TTGAACAGCG | TGGAATAATT | TTTTTCATAGT | GAGATGGACC | ATTCCATTTG | 1250 |
| TTTCTAACTT | CAAGTGATCA | ATGTAATTTA | GATTGATAAT | TTCTGATTTT | 1300 |
| GAAATACGCA | CGAATATTGA | ACCGACAAGC | TCTTCAATTT | GGTAAAGTCG | 1350 |

| | | | | | |
|-------------|------------|------------|-------------|-------------|------|
| CTGATAAAGT | TTTAAAGCTT | TATTATTCAT | TGTTATCGCA | TACCTGTTTA | 1400 |
| TCTTCTACTA | TGAACTGTGC | AATTTGTTCT | AGATCAATTG | GGTAAACATG | 1450 |
| ATGGTTCTGT | TGCAAAGTAA | AAAAATATAG | CTAACCCTA | ATTTATCATG | 1500 |
| TCAGTGTTTCG | CTTAACTTGC | TAGCATGATG | CTAATTTTCGT | GGCATGGCGA | 1550 |
| AAATCCGTAG | ATCTGATGAG | ACCTGCGGTT | CTTTTTATAT | AGAGCGTAAA | 1600 |
| TACATTCAAT | ACCTTTTAAA | GTATTCTTTG | CTGTATTGAT | ACTTTGATAC | 1650 |
| CTTGTCCTTC | TTACTTTAAT | ATGACGGTGA | TCTTGCTCAA | TGAGGTTATT | 1700 |
| CAGATATTTT | GATGTACAAT | GACAGTCAGG | TTTAAGTTTA | AAAGCTTTAA | 1750 |
| TTACTTTAGC | CATTGCTACC | TTCGTTGAAG | GTGCCTGATC | TGTAATTACC | 1800 |
| TTTTGAGGTT | TACCAAATTG | TTTAATGAGA | CGTTTGATAA | ACGCATATGC | 1850 |
| TGAATGATTA | TCTCGTTGCT | TACGCAACCA | AATATCTAAT | GTATGTCCTT | 1900 |
| CTGCATCAAT | GGCACGATAT | AAATAGCTCC | ATTTTCCTTT | TATTTTGATG | 1950 |
| TACGTCTCAT | CAATACGCCA | TTTGTAATAA | GCTTTTTTTAT | GCTTTTTTCTT | 2000 |
| CCAAATTTGA | TACAAAATTG | GGGCATATTC | TTGAACCCAA | CGGTAGACCG | 2050 |
| TTGAATGATG | AACGTTTACA | CCACGTTCCC | TTAATATTTT | AGATATATCA | 2100 |
| CGATAACTCA | ATGTATATCT | TA | | | 2122 |

2) INFORMATION FOR SEQ ID NO: 52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

GATAGACTAA TTATCTTCAT C**21**

2) INFORMATION FOR SEQ ID NO: 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

CAGACTGTGG ACAAACCTGAT T**21**

2) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

39/125

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

TGAGATCATC TACATCTTTA

20

2) INFORMATION FOR SEQ ID NO: 55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

GGATCAAAAG CTACTAAATC

20

2) INFORMATION FOR SEQ ID NO: 56

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

ATGCTCTTTG TTTTGCAGCA

20

2) INFORMATION FOR SEQ ID NO: 57

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

ATGAAAGACT GCGGAGGCTA ACT

23

2) INFORMATION FOR SEQ ID NO: 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

ATATTCTAGA TCATCAATAG TTG

23

2) INFORMATION FOR SEQ ID NO: 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

AAGAATTGAA CCAACGCATG A

21

2) INFORMATION FOR SEQ ID NO: 60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

GTTCAAGCCC AGAAGCGATG T**21****2) INFORMATION FOR SEQ ID NO: 61****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 23 bases
- (B) TYPE:** Nucleic acid
- (C) STRANDEDNESS:** Single
- (D) TOPOLOGY:** Linear

(ii) MOLECULE TYPE: DNA**(xi) SEQUENCE DESCRIPTION:** SEQ ID NO: 61**TCGGGCATAA ATGTCAGGAA AAT****23****2) INFORMATION FOR SEQ ID NO: 62****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 21 bases
- (B) TYPE:** Nucleic acid
- (C) STRANDEDNESS:** Single
- (D) TOPOLOGY:** Linear

(ii) MOLECULE TYPE: DNA**(xi) SEQUENCE DESCRIPTION:** SEQ ID NO: 62**AAACGACATG AAAATCACCA T****21****2) INFORMATION FOR SEQ ID NO: 63****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH:** 33 bases
- (B) TYPE:** Nucleic acid
- (C) STRANDEDNESS:** Single
- (D) TOPOLOGY:** Linear

(ii) MOLECULE TYPE: DNA**(xi) SEQUENCE DESCRIPTION:** SEQ ID NO: 63**TTATTAGGTA AACCAGCAGT AAGTGAACAA CCA****33**

2) INFORMATION FOR SEQ ID NO: 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

GGATCAAACG GCCTGCACA**19**

2) INFORMATION FOR SEQ ID NO: 65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

CACAGAAATG TAATTTTGGA ATGAGG**26**

2) INFORMATION FOR SEQ ID NO: 66

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

GTCAAAAATC ATGAACCTCA TTA CTTATG**29**

2) INFORMATION FOR SEQ ID NO: 67

(i) SEQUENCE CHARACTERISTICS:

43/125

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

ATTTCATATA TGTAATTCCT CCACATCTC

29

2) INFORMATION FOR SEQ ID NO: 68

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

TCTACGGATT TTCGCCATGC

20

2) INFORMATION FOR SEQ ID NO: 69

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

AACAGGTGAA TTATTAGCAC TTGTAAG

27

2) INFORMATION FOR SEQ ID NO: 70

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

ATCAAATGAT GCGGGTTGTG T

21

2) INFORMATION FOR SEQ ID NO: 71

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

TCATTGGCGG ATCAAACGG

19

2) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

ACAACGCAGT AACTACGCAC TA

22

2) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

TAACTACGCA CTATCATTCA GC**22****2) INFORMATION FOR SEQ ID NO: 74****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 22 bases**
- (B) TYPE: Nucleic acid**
- (C) STRANDEDNESS: Single**
- (D) TOPOLOGY: Linear**

(ii) MOLECULE TYPE: DNA**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74****ACATCAAATG ATGCGGGTTG TG****22****2) INFORMATION FOR SEQ ID NO: 75****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 22 bases**
- (B) TYPE: Nucleic acid**
- (C) STRANDEDNESS: Single**
- (D) TOPOLOGY: Linear**

(ii) MOLECULE TYPE: DNA**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75****TCAAATGATG CGGGTTGTGT TA****22****2) INFORMATION FOR SEQ ID NO: 76****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 24 bases**
- (B) TYPE: Nucleic acid**
- (C) STRANDEDNESS: Single**
- (D) TOPOLOGY: Linear**

(ii) MOLECULE TYPE: DNA**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76****CAAATGATGC GGGTTGTGTT AATT****24**

2) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

CTACTATGAA CTGTGCAATT TGTTC

26

2) INFORMATION FOR SEQ ID NO: 78

- (i) (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 8325
- (C) ACCESSION NUMBER: Extracted from X52593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

| | | | | | |
|------------|------------|-------------|------------|------------|-----|
| ATGAAAAGA | TAAAAATTGT | TCCACTTATT | TTAATAGTTG | TAGTTGTCGG | 50 |
| GTTTGGTATA | TATTTTATG | CTTCAAAGA | TAAAGAAATT | AATAATACTA | 100 |
| TTGATGCAAT | TGAAGATAAA | AATTTCAAAC | AAGTTTATAA | AGATAGCAGT | 150 |
| TATATTTCTA | AAAGCGATAA | TGGTGAAGTA | GAAATGACTG | AACGTCCGAT | 200 |
| AAAAATATAT | AATAGTTTAG | GCGTTAAAGA | TATAAACATT | CAGGATCGTA | 250 |
| AAATAAAAAA | AGTATCTAAA | AATAAAAAAC | GAGTAGATGC | TCAATATAAA | 300 |
| ATTAAACAA | ACTACGGTAA | CATTGATCGC | AACGTTCAAT | TTAATTTTGT | 350 |
| TAAAGAAGAT | GGTATGTGGA | AGTTAGATTG | GGATCATAGC | GTCATTATTC | 400 |
| CAGGAATGCA | GAAAGACCAA | AGCATACATA | TTGAAAATTT | AAAATCAGAA | 450 |
| CGTGGTAAAA | TTTTAGACCG | AAACAATGTG | GAATTGGCCA | ATACAGGAAC | 500 |
| ACATATGAGA | TTAGGCATCG | TTCCAAAGAA | TGTATCTAAA | AAAGATTATA | 550 |
| AAGCAATCGC | TAAAGAACTA | AGTATTTCTG | AAGACTATAT | CAACAACAAA | 600 |
| TGGATCAAAA | TTGGGTACAA | GATGATACCT | TCGTTCCACT | TTAAAACCGT | 650 |
| TAAAAAAATG | GATGAATATT | TAAGTGATTT | CGCAAAAAAA | TTTCATCTTA | 700 |
| CAACTAATGA | AACAGAAAGT | CGTAACTATC | CTCTAGAAAA | AGCGACTTCA | 750 |
| CATCTATTAG | GTTATGTTGG | TCCCATTAAAC | TCTGAAGAAT | TAAAACAAAA | 800 |
| AGAATATAAA | GGCTATAAAG | ATGATGCAGT | TATTGGTAAA | AAGGGACTCG | 850 |
| AAAAACTTTA | CGATAAAAAG | CTCCAACATG | AAGATGGCTA | TCGTGTCACA | 900 |
| ATCGTTGACG | ATAATAGCAA | TACAATCGCA | CATACATTAA | TAGAGAAAAA | 950 |

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GAAAAAAGAT | GGCAAAGATA | TTCAACTAAC | TATTGATGCT | AAAGTTCAAA | 1000 |
| AGAGTATTTA | TAACAACATG | AAAAATGATT | ATGGCTCAGG | TACTGCTATC | 1050 |
| CACCCTCAAA | CAGGTGAATT | ATTAGCACTT | GTAAGCACAC | CTTCATATGA | 1100 |
| CGTCTATCCA | TTTATGTATG | GCATGAGTAA | CGAAGAATAT | AATAAATTAA | 1150 |
| CCGAAGATAA | AAAAGAACCT | CTGCTCAACA | AGTTCCAGAT | TACAACTTCA | 1200 |
| CCAGGTTCAA | CTCAAAAAAT | ATTAACAGCA | ATGATTGGGT | TAAATAACAA | 1250 |
| AACATTAGAC | GATAAAACAA | GTTATAAAAT | CGATGGTAAA | GGTTGGCAAA | 1300 |
| AAGATAAATC | TTGGGGTGGT | TACAACGTTA | CAAGATATGA | AGTGGTAAAT | 1350 |
| GGTAATATCG | ACTTAAAACA | AGCAATAGAA | TCATCAGATA | ACATTTTCTT | 1400 |
| TGCTAGAGTA | GCACTCGAAT | TAGGCAGTAA | GAAATTTGAA | AAAGGCATGA | 1450 |
| AAAAACTAGG | TGTTGGTGAA | GATATACCAA | GTGATTATCC | ATTTTATAAT | 1500 |
| GCTCAAATTT | CAAACAAAAA | TTTAGATAAT | GAAATATTAT | TAGCTGATTC | 1550 |
| AGGTTACGGA | CAAGGTGAAA | TACTGATTAA | CCCAGTACAG | ATCCTTTCAA | 1600 |
| TCTATAGCGC | ATTAGAAAAT | AATGGCAATA | TTAACGCACC | TCACCTATTA | 1650 |
| AAAGACACGA | AAAACAAAGT | TTGGAAGAAA | AATATTATTT | CCAAAGAAAA | 1700 |
| TATCAATCTA | TTAAATGATG | GTATGCAACA | AGTCGTAAAT | AAAACACATA | 1750 |
| AAGAAGATAT | TTATAGATCT | TATGCAAAC | TAATTGGCAA | ATCCGGTACT | 1800 |
| GCAGAACTCA | AAATGAAACA | AGGAGAAAGT | GGCAGACAAA | TTGGGTGGTT | 1850 |
| TATATCATAT | GATAAAGATA | ATCCAAACAT | GATGATGGCT | ATTAATGTTA | 1900 |
| AAGATGTACA | AGATAAAGGA | ATGGCTAGCT | ACAATGCCAA | AATCTCAGGT | 1950 |
| AAAGTGTATG | ATGAGCTATA | TGAGAACGGT | AATAAAAAAT | ACGATATAGA | 2000 |
| TGAATAA | | | | | 2007 |

2) INFORMATION FOR SEQ ID NO: 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79

CAAATATTAT CTCGTAATTT ACCTTGTTT

29

2) INFORMATION FOR SEQ ID NO: 80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80

CTCTGCTTTA TATTATAAAA TTACGGCTG**29****2) INFORMATION FOR SEQ ID NO: 81****(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA**(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81****ATTGCTGTTA ATATTTTTTG AGTTGAA****27****2) INFORMATION FOR SEQ ID NO: 82**

- (i) (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA**(vi) ORIGINAL SOURCE:**

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 10442
- (C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGAAAAGA | TAAAAATTGT | TCCACTTATT | TTAATAGTTG | TAGTTGTCGG | 50 |
| GTTTGGTATA | TATTTTATG | CTTCAAAAGA | TAAAGAAATT | AATAATACTA | 100 |
| TTGATGCAAT | TGAAGATAAA | AATTTCAAAC | AAGTTTATAA | AGATAGCAGT | 150 |
| TATATTTCTA | AAAGCGATAA | TGGTGAAGTA | GAAATGACTG | AACGTCCGAT | 200 |
| AAAAATATAT | AATAGTTTAG | GCGTTAAAGA | TATAAACATT | CAGGATCGTA | 250 |
| AAATAAAAAA | AGTATCTAAA | AATAAAAAAC | GAGTAGATGC | TCAATATAAA | 300 |
| ATTAAACAA | ACTACGGTAA | CATTGATCGC | AACGTTCAAT | TTAATTTTGT | 350 |
| TAAAGAAGAT | GGTATGTGGA | AGTTAGATTG | GGATCATAGC | GTCATTATTC | 400 |
| CAGGAATGCA | GAAAGACCAA | AGCATAcata | TTGAAAATTT | AAAATCAGAA | 450 |
| CGTGGTAAAA | TTTTAGACCG | AAACAATGTG | GAATTGGCCA | ATACAGGAAC | 500 |
| AGCATATGAG | ATAGGCATCG | TTCCAAAGAA | TGTATCTAAA | AAAGATTATA | 550 |
| AAGCAATCGC | TAAAGAACTA | AGTATTTCTG | AAGACTATAT | CAAACAACAA | 600 |
| ATGGATCAAA | ATTGGGTACA | AGATGATACC | TTCGTTCCAC | TTAAAACCGT | 650 |
| TAAAAAAATG | GATGAATATT | TAAGTGATTT | CGCAAAAAAA | TTTCATCTTA | 700 |
| CAACTAATGA | AACAGAAAGT | CGTAACTATC | CTCTAGAAAA | AGCGACTTCA | 750 |

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| CATCTATTAG | GTTATGTTGG | TCCCATTAAAC | TCTGAAGAAT | TAAAACAAAA | 800 |
| AGAATATAAA | GGCTATAAAG | ATGATGCAGT | TATTGGTAAA | AAGGGACTCG | 850 |
| AAAAACTTTA | CGATAAAAAG | CTCCAACATG | AAGATGGCTA | TCGTGTCACA | 900 |
| ATCGTTGACG | ATAATAGCAA | TACAATCGCA | CATACATTAA | TAGAGAAAAA | 950 |
| GAAAAAAGAT | GGCAAAGATA | TTCAACTAAC | TATTGATGCT | AAAGTTCAAA | 1000 |
| AGAGTATTTA | TAACAACATG | AAAAATGATT | ATGGCTCAGG | TACTGCTATC | 1050 |
| CACCCTCAAA | CAGGTGAATT | ATTAGCACTT | GTAAGCACAC | CTTCATATGA | 1100 |
| CGTCTATCCA | TTTATGTATG | GCATGAGTAA | CGAAGAATAT | AATAAATTAA | 1150 |
| CCGAAGATAA | AAAAGAACCT | CTGCTCAACA | AGTTCCAGAT | TACAACCTCA | 1200 |
| CCAGGTTCAA | CTCAAAAAAT | ATTAACAGCA | ATGATTGGGT | TAAATAACAA | 1250 |
| AACATTAGAC | GATAAAACAA | GTTATAAAAT | CGATGGTAAA | GGTTGGCAAA | 1300 |
| AAGATAAATC | TTGGGGTGGT | TACAACGTTA | CAAGATATGA | AGTGGTAAAT | 1350 |
| GGTAATATCG | ACTTAAAACA | AGCAATAGAA | TCATCAGATA | ACATTTTCTT | 1400 |
| TGCTAGAGTA | GCACTCGAAT | TAGGCAGTAA | GAAATTTGAA | AAAGGCATGA | 1450 |
| AAAAACTAGG | TGTTGGTGAA | GATATACCAA | GTGATTATCC | ATTTTATAAT | 1500 |
| GCTCAAATTT | CAAACAAAAA | TTTAGATAAT | GAAATATTAT | TAGCTGATTC | 1550 |
| AGGTTACGGA | CAAGGTGAAA | TACTGATTAA | CCCAGTACAG | ATCCTTTCAA | 1600 |
| TCTATAGCGC | ATTAGAAAAT | AATGGCAATA | TTAACGCACC | TCACTTATTA | 1650 |
| AAAGACACGA | AAAACAAAGT | TTGGAAGAAA | AATATTATTT | CCAAAGAAAA | 1700 |
| TATCAATCTA | TTAACTGATG | GTATGCAACA | AGTCGTAAAT | AAAACACATA | 1750 |
| AAGAAGATAT | TTATAGATCT | TATGCAAAC | TAATTGGCAA | ATCCGGTACT | 1800 |
| GCAGAACTCA | AAATGAAACA | AGGAGAAACT | GGCAGACAAA | TTGGGTGGTT | 1850 |
| TATATCATAT | GATAAAGATA | ATCCAAACAT | GATGATGGCT | ATTAATGTTA | 1900 |
| AAGATGTACA | AGATAAAGGA | ATGGCTAGCT | ACAATGCCAA | AATCTCAGGT | 1950 |
| AAAGTGTATG | ATGAGCTATA | TGAGAACGGT | AATAAAAAAT | ACGATATAGA | 2000 |
| TGAATAA | | | | | 2007 |

2) INFORMATION FOR SEQ ID NO: 83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83

CCCACCCAC ATCAAATGAT GCGGGTTGTG GGTGGG

36

2) INFORMATION FOR SEQ ID NO: 84

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84

CCCGCGCGTA GTTACTGCGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 85

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85

GTTTTTATCA CCATATTGAA TTTATAC

27

2) INFORMATION FOR SEQ ID NO: 86

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86

ATTACTTGA AAGACTGCGG AGGAG

25

2) INFORMATION FOR SEQ ID NO: 87

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87

TGTTTGAGCT TCCACAGCTA TTTC

24

2) INFORMATION FOR SEQ ID NO: 88

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88

CCCTATAATT CCAATTATTG CACTAAC

27

2) INFORMATION FOR SEQ ID NO: 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89

ATGAGGAGAT AATAATTGG AGGGT

25

2) INFORMATION FOR SEQ ID NO: 90

- (i) (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: N315
- (C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| ATGAAAAAGA | TAAAAATTGT | TCCACTTATT | TTAATAGTTG | TAGTTGTCGG | 50 |
| GTTTGGTATA | TATTTTATG | CTTCCAAAGA | TAAAGAAATT | AATAATACTA | 100 |
| TTGATGCAAT | TGAAGATAAA | AATTTCAAAC | AAGTTTATAA | AGATAGCAGT | 150 |
| TATATTTCTA | AAAGCGATAA | TGGTGAAGTA | GAAATGACTG | AACGTCCGAT | 200 |
| AAAAATATAT | AATAGTTTAG | GCGTTAAAGA | TATAAACATT | CAGGATCGTA | 250 |
| AAATAAAAAA | AGTATCTAAA | AATAAAAAAC | GAGTAGATGC | TCAATATAAA | 300 |
| ATTAAAACAA | ACTACGGTAA | CATTGATCGC | AACGTTCAAT | TTAATTTTGT | 350 |
| TAAAGAAGAT | GGTATGTGGA | AGTTAGATTG | GGATCATAGC | GTCATTATTC | 400 |
| CAGGAATGCA | GAAAGACCAA | AGCATAACATA | TTGAAAATTT | AAAATCAGAA | 450 |
| CGTGGTAAAA | TTTTAGACCG | AAACAATGTG | GAATTGGCCA | ATACAGGAAC | 500 |
| AGCATATGAG | ATAGGCATCG | TTCCAAAGAA | TGTATCTAAA | AAAGATTATA | 550 |
| AAGCAATCGC | TAAAGAACTA | AGTATTTCTG | AAGACTATAT | CAAACAACAA | 600 |
| ATGGATCAAA | ATTGGGTACA | AGATGATACC | TTCGTTCCAC | TTAAAACCGT | 650 |
| TAAAAAAATG | GATGAATATT | TAAGTGATTT | CGCAAAAAAA | TTTCATCTTA | 700 |
| CAACTAATGA | AACAGAAAGT | CGTAACTATC | CTCTAGGAAA | AGCGACTTCA | 750 |
| CATCTATTAG | GTTATGTTGG | TCCCATTAAC | TCTGAAGAAT | TAAAACAAAA | 800 |
| AGAATATAAA | GGCTATAAAG | ATGATGCAGT | TATTGGTAAA | AAGGGACTCG | 850 |
| AAAAACTTTA | CGATAAAAAG | CTCCAACATG | AAGATGGCTA | TCGTGTCACA | 900 |
| ATCGTTGACG | ATAATAGCAA | TACAATCGCA | CATACATTAA | TAGAGAAAAA | 950 |
| GAAAAAAGAT | GGCAAAGATA | TTCAACTAAC | TATTGATGCT | AAAGTTCAAA | 1000 |
| AGAGTATTTA | TAACAACATG | AAAAATGATT | ATGGCTCAGG | TACTGCTATC | 1050 |
| CACCCTCAAA | CAGGTGAATT | ATTAGCACTT | GTAAGCACAC | CTTCATATGA | 1100 |
| CGTCTATCCA | TTTATGTATG | GCATGAGTAA | CGAAGAATAT | AATAAATTAA | 1150 |
| CCGAAGATAA | AAAAGAACCT | CTGCTCAACA | AGTTCCAGAT | TACAACTTCA | 1200 |
| CCAGGTTCAA | CTCAAAAAAT | ATTAACAGCA | ATGATTGGGT | TAAATAACAA | 1250 |
| AACATTAGAC | GATAAAACAA | GTTATAAAAT | CGATGGTAAA | GGTTGGCAAA | 1300 |
| AAGATAAATC | TTGGGGTGGT | TACAACGTTA | CAAGATATGA | AGTGGTAAAT | 1350 |
| GGTAATATCG | ACTTAAAACA | AGCAATAGAA | TCATCAGATA | ACATTTTCTT | 1400 |
| TGCTAGAGTA | GCACTCGAAT | TAGGCAGTAA | GAAATTTGAA | AAAGGCATGA | 1450 |
| AAAAACTAGG | TGTTGGTGAA | GATATACCAA | GTGATTATCC | ATTTTATAAT | 1500 |
| GCTCAAATTT | CAAACAAAAA | TTTAGATAAT | GAAATATTAT | TAGCTGATTC | 1550 |
| AGGTTACGGA | CAAGGTGAAA | TACTGATTAA | CCCAGTACAG | ATCCTTTCAA | 1600 |
| TCTATAGCGC | ATTAGAAAAT | AATGGCAATA | TTAACGCACC | TCACTTATTA | 1650 |
| AAAGACACGA | AAAACAAAGT | TTGGAAGAAA | AATATTATTT | CCAAAGAAAA | 1700 |
| TATCAATCTA | TTAACTGATG | GTATGCAACA | AGTCGTAAAT | AAAACACATA | 1750 |
| AAGAAGATAT | TTATAGATCT | TATGCAAAC | TAATTGGCAA | ATCCGGTACT | 1800 |
| GCAGAACTCA | AAATGAAACA | AGGAGAAACT | GGCAGACAAA | TTGGGTGGTT | 1850 |
| TATATCATAT | GATAAAGATA | ATCCAAACAT | GATGATGGCT | ATTAATGTTA | 1900 |
| AAGATGTACA | AGATAAAGGA | ATGGCTAGCT | ACAATGCCAA | AATCTCAGGT | 1950 |
| AAAGTGTATG | ATGAGCTATA | TGAGAACGGT | AATAAAAAAT | ACGATATAGA | 2000 |
| TGAATAA | | | | | 2007 |

2) INFORMATION FOR SEQ ID NO: 91

- (i) (A) LENGTH: 2007 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: 85/2082

(C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| ATGAAAAAGA | TAAAAATTGT | TCCACTTATT | TTAATAGTTG | TAGTTGTCGG | 50 |
| GTTTGGTATA | TATTTTATG | CTTCAAAGA | TAAAGAAATT | AATAATACTA | 100 |
| TTGATGCAAT | TGAAGATAAA | AATTTCAAAC | AAGTTTATAA | AGATAGCAGT | 150 |
| TATATTTCTA | AAAGCGATAA | TGGTGAAGTA | GAAATGACTG | AACGTCCGAT | 200 |
| AAAAATATAT | AATAGTTTAG | GCGTTAAAGA | TATAAACATT | CAGGATCGTA | 250 |
| AAATAAAAAA | AGTATCTAAA | AATAAAAAAC | GAGTAGATGC | TCAATATAAA | 300 |
| ATTAAAACAA | ACTACGGTAA | CATTGATCGC | AACGTTCAAT | TTAATTTTGT | 350 |
| TAAAGAAGAT | GGTATGTGGA | AGTTAGATTG | GGATCATAGC | GTCATTATTC | 400 |
| CAGGAATGCA | GAAAGACCAA | AGCATACATA | TTGAAAATTT | AAAATCAGAA | 450 |
| CGTGGTAAAA | TTTTAGACCG | AAACAATGTG | GAATTGGCCA | ATACAGGAAC | 500 |
| AGCATATGAG | ATAGGCATCG | TTCCAAAGAA | TGTATCTAAA | AAAGATTATA | 550 |
| AAGCAATCGC | TAAAGAACTA | AGTATTTCTG | AAGACTATAT | CAAACAACAA | 600 |
| ATGGATCAAA | AGTGGGTACA | AGATGATACC | TTCGTTCCAC | TTAAAACCGT | 650 |
| TAAAAAAATG | GATGAATATT | TAAGTGATTT | CGCAAAAAAA | TTTCATCTTA | 700 |
| CAACTAATGA | AACAGAAAGT | CGTAACTATC | CTCTAGAAAA | AGCGACTTCA | 750 |
| CATCTATTAG | GTTATGTTGG | TCCCATTAAAC | TCTGAAGAAT | TAAAACAAAA | 800 |
| AGAATATAAA | GGCTATAAAG | ATGATGCAGT | TATTGGTAAA | AAGGGACTCG | 850 |
| AAAAACTTTA | CGATAAAAAG | CTCCAACATG | AAGATGGCTA | TCGTGTCACA | 900 |
| ATCGTTGACG | ATAATAGCAA | TACAATCGCA | CATACATTAA | TAGAGAAAAA | 950 |
| GAAAAAAGAT | GGCAAAGATA | TTCAACTAAC | TATTGATGCT | AAAGTTCAAA | 1000 |
| AGAGTATTTA | TAACAACATG | AAAAATGATT | ATGGCTCAGG | TACTGCTATC | 1050 |
| CACCCTCAAA | CAGGTGAATT | ATTAGCACTT | GTAAGCACAC | CTTCATATGA | 1100 |
| CGTCTATCCA | TTTATGTATG | GCATGAGTAA | CGAAGAATAT | AATAAATTAA | 1150 |
| CCGAAGATAA | AAAAGAACCT | CTGCTCAACA | AGTTCCAGAT | TACAACTTCA | 1200 |
| CCAGGTTCAA | CTCAAAAAAT | ATTAACAGCA | ATGATTGGGT | TAAATAACAA | 1250 |
| AACATTAGAC | GATAAAACAA | GTTATAAAAT | CGATGGTAAA | GGTTGGCAAA | 1300 |
| AAGATAAATC | TTGGGGTGGT | TACAACGTTA | CAAGATATGA | AGTGGTAAAT | 1350 |
| GGTAATATCG | ACTTAAAACA | AGCAATAGAA | TCATCAGATA | ACATTTTCTT | 1400 |
| TGCTAGAGTA | GCACTCGAAT | TAGGCAGTAA | GAAATTTGAA | AAAGGCATGA | 1450 |
| AAAAACTAGG | TGTTGGTGAA | GATATACCAA | GTGATTATCC | ATTTTATAAT | 1500 |
| GCTCAAATTT | CAAACAAAAA | TTTAGATAAT | GAAATATTAT | TAGCTGATTC | 1550 |
| AGGTTACGGA | CAAGGTGAAA | TACTGATTAA | CCCAGTACAG | ATCCTTTCAA | 1600 |
| TCTATAGCGC | ATTAGAAAAT | AATGGCAATA | TTAACGCACC | TCACTTATTA | 1650 |
| AAAGACACGA | AAAACAAAGT | TTGGAAGAAA | AATATTATTT | CCAAAGAAAA | 1700 |
| TATCAATCTA | TTAACTGATG | GTATGCAACA | AGTCGTAAAT | AAAACACATA | 1750 |
| AAGAAGATAT | TTATAGATCT | TATGCAAAC | TAATTGGCAA | ATCCGGTACT | 1800 |
| GCAGAACTCA | AAATGAAACA | AGGAGAAACT | GGCAGACAAA | TTGGGTGGTT | 1850 |
| TATATCATAT | GATAAAGATA | ATCCAAACAT | GATGATGGCT | ATTAATGTTA | 1900 |
| AAGATGTACA | AGATAAAGGA | ATGGCTAGCT | ACAATGCCAA | AATCTCAGGT | 1950 |
| AAAGTGTATG | ATGAGCTATA | TGAGAACGGT | AATAAAAAAT | ACGATATAGA | 2000 |
| TGAATAA | | | | | 2007 |

2) INFORMATION FOR SEQ ID NO: 92

- (i) (A) LENGTH: 675 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 10442
- (C) ACCESSION NUMBER: Extracted from AB033763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92

| | |
|---------------------------------------------------------|-----|
| ATGAACTATT TCAGATATAA ACAATTTAAC AAGGATGTTA TCACTGTAGC | 50 |
| CGTTGGCTAC TATCTAAGAT ATACATTGAG TTATCGTGAT ATATCTGAAA | 100 |
| TATTAAGGGA ACGTGGTGTA AACGTTTCATC ATTCAACGGT CTACCGTTGG | 150 |
| GTTCAAGAAT ATGCCCCAAT TTTGTATCAA ATTTGGAAGA AAAAGCATAA | 200 |
| AAAAGCTTAT TACAAATGGC GTATTGATGA GACGTACATC AAAATAAAAG | 250 |
| GAAAATGGAG CTATTTATAT CGTGCCATTG ATGCAGAGGG ACATACATTA | 300 |
| GATATTTGGT TGCGTAAGCA ACGAGATAAT CATTTCAGCAT ATGCGTTTAT | 350 |
| CAAACGTCTC ATTAAACAAT TTGGTAAACC TCAAAAGGTA ATTACAGATC | 400 |
| AGGCACCTTC AACGAAGGTA GCAATGGCTA AAGTAATTAA AGCTTTTAAA | 450 |
| CTTAAACCTG ACTGTCATTG TACATCGAAA TATCTGAATA ACCTCATTGA | 500 |
| GCAAGATCAC CGTCATATTA AAGTAAGAAA GACAAGGTAT CAAAGTATCA | 550 |
| ATACAGCAAA GAATACTTTA AAAGGTATTG AATGTATTTA CGCTCTATAT | 600 |
| AAAAAGAACC GCAGGTCTCT TCAGATCTAC GGATTTTTCGC CATGCCACGA | 650 |
| AATTAGCATC ATGCTAGCAA GTTAA | 675 |

2) INFORMATION FOR SEQ ID NO: 93

- (i) (A) LENGTH: 675 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: N315
- (C) ACCESSION NUMBER: Extracted from D86934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93

| | |
|--------------------------------------------------------|----|
| ATGAACTATT TCAGATATAA ACAATTTAAC AAGGATGTTA TCACTGTAGC | 50 |
|--------------------------------------------------------|----|

| | | | | | |
|------------|------------|-------------|------------|-------------|-----|
| CGTTGGCTAC | TATCTAAGAT | ATACATTGAG | TTATCGTGAT | ATATCTGAAA | 100 |
| TATTAAGGGA | ACGTGGTGTA | AACGTTTCATC | ATTCAACGGT | CTACCGTTGG | 150 |
| GTTCAAGAAT | ATGCCCCAAT | TTTGTATCAA | ATTTGGAAGA | AAAAGCATAA | 200 |
| AAAAGCTTAT | TACAAATGGC | GTATTGATGA | GACGTACATC | AAAATAAAAAG | 250 |
| GAAAATGGAG | CTATTTATAT | CGTGCCATTG | ATGCAGAGGG | ACATACATTA | 300 |
| GATATTTGGT | TGCGTAAGCA | ACGAGATAAT | CATTCAGCAT | ATGCGTTTAT | 350 |
| CAAACGTCTC | ATTAAACAAT | TTGGTAAACC | TCAAAAGGTA | ATTACAGATC | 400 |
| AGGCACCTTC | AACGAAGGTA | GCAATGGCTA | AAGTAATTAA | AGCTTTTAAA | 450 |
| CTTAAACCTG | ACTGTCATTG | TACATCGAAA | TATCTGAATA | ACCTCATTGA | 500 |
| GCAAGATCAC | CGTCATATTA | AAGTAAGAAA | GACAAGGTAT | CAAAGTATCA | 550 |
| ATACAGCAAA | GAATACTTTA | AAAGGTATTG | AATGTATTTA | CGCTCTATAT | 600 |
| AAAAAGAACC | GCAGGTCTCT | TCAGATCTAC | GGATTTTCGC | CATGCCACGA | 650 |
| AATTAGCATC | ATGCTAGCAA | GTAA | | | 675 |

2) INFORMATION FOR SEQ ID NO: 94

- (i) (A) LENGTH: 675 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: HUC19
- (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94

| | | | | | |
|------------|------------|-------------|------------|-------------|-----|
| ATGAACTATT | TCAGATATAA | ACAATTTAAC | AAGGATGTTA | TCACTGTAGC | 50 |
| CGTTGGCTAC | TATCTAAGAT | ATACATTGAG | TTATCGTGAT | ATATCTGAAA | 100 |
| TATTAAGGGA | ACGTGGTGTA | AACGTTTCATC | ATTCAACGGT | CTACCGTTGG | 150 |
| GTTCAAGAAT | ATGCCCCAAT | TTTGTATCAA | ATTTGGAAGA | AAAAGCATAA | 200 |
| AAAAGCTTAT | TACAAATGGC | GTATTGATGA | GACGTACATC | AAAATAAAAAG | 250 |
| GAAAATGGAG | CTATTTATAT | CGTGCCATTG | ATGCAGAGGG | ACATACATTA | 300 |
| GATATTTGGT | TGCGTAAGCA | ACGAGTTAAT | CATTCAGCAT | ATGCGTTTAT | 350 |
| CAAACGTCTC | ATTAAACAAT | TTGGTAAACC | TCAAAAGGTA | ATTACAGATC | 400 |
| AGGCACCTTC | AACGAAGGTA | GCAATGGCTA | AAGTAATTAA | AGCTTTTAAA | 450 |
| CTTAAACCTG | ACTGTCATTG | TACATCGAAA | TATCTGAATA | ACCTCATTGA | 500 |
| GCAAGATCAC | CGTCATATTA | AAGTAAGAAA | GACAAGGTAT | CAAAGTATCA | 550 |
| ATACAGCAAA | GAATACTTTA | AAAGGTATTG | AATGTATTCA | CGCTCTATAT | 600 |
| AAAAAGAACC | GCAGGTCTCT | TCAGATCTAC | GGATTTTCGC | CATGCCACGA | 650 |
| AATTAGCATC | ATGCTAGCAA | GTAA | | | 675 |

2) INFORMATION FOR SEQ ID NO: 95

- (i) (A) LENGTH: 675 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: NCTC 8325
- (C) ACCESSION NUMBER: Extracted from X53818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95

| | | | | | |
|------------|------------|-------------|------------|-------------|-----|
| ATGAACTATT | TCAGATATAA | ACAATTTAAC | AAGGATGTTA | TCACTGTAGC | 50 |
| CGTTGGCTAC | TATCTAAGAT | ATACATTGAG | TTATCGTGAT | ATATCTGAAA | 100 |
| TATTAAGGGA | ACGTGGTGTA | AACGTTTCATC | ATTCAACGGT | CTACCGTTGG | 150 |
| GTTCAAGAAT | ATGCCCCAAT | TTTGTATCAA | ATTTGGAAGA | AAAAGCATAA | 200 |
| AAAAGCTTAT | TACAAATGGC | GTATTGATGA | GACGTACATC | AAAATAAAAAG | 250 |
| GAAAATGGAG | CTATTTATAT | CGTGCCATTG | ATGCAGAGGG | ACATACATTA | 300 |
| GATATTTGGT | TGCGTAAGCA | ACGAGATAAT | CATTCAGCAT | ATGCGTTTAT | 350 |
| CAAACGTCTC | ATTAAACAAT | TTGGTAAACC | TCAAAAGGTA | ATTACAGATC | 400 |
| AGGCACCTTC | AACGAAGGTA | GCAATGGCTA | AAGTAATTAA | AGCTTTTAAA | 450 |
| CTTAAACCTG | ACTGTCATTG | TACATCGAAA | TATCTGAATA | ACCTCATTGA | 500 |
| GCAAGATCAC | CGTCATATTA | AAGTAAGAAA | GACAAGGTAT | CAAAGTATCA | 550 |
| ATACAGCAAA | GAATACTTTA | AAAGGTATTG | AATGTATTTA | CGCTCTATAT | 600 |
| AAAAAGAACC | GCAGGTCTCT | TCAGATCTAC | GGATTTTCGC | CATGCCACGA | 650 |
| AATTAGCATC | ATGCTAGCAA | GTAA | | | 675 |

2) INFORMATION FOR SEQ ID NO: 96

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96

GTAAAGTGTA TGATGAGCTA TATGAGAA

28

2) INFORMATION FOR SEQ ID NO: 97

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

57/125

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97

GCTGAAAAAA CCGCATCATT TRTGRTA

27

2) INFORMATION FOR SEQ ID NO: 98

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98

TTTAGTTTTA TTTATGATAC GCTTCTCCA

29

2) INFORMATION FOR SEQ ID NO: 99

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99

GCTGAAAAAA CCGCATCATT TATGATA

27

2) INFORMATION FOR SEQ ID NO: 100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100

CTATGTCAAA AATCATGAAC CTCATTAC

28

2) INFORMATION FOR SEQ ID NO: 101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101

GGAGGCTAAC TATGTCAAAA ATC

23

2) INFORMATION FOR SEQ ID NO: 102

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102

CTCTATAAAC ATCGTATGAT ATTGC

25

2) INFORMATION FOR SEQ ID NO: 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103

ACCAAACGAC ATGAAAATCA

20

2) INFORMATION FOR SEQ ID NO: 104

- (i) (A) LENGTH: 1256 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2082
- (C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104

| | | | | | |
|------------|-------------|-------------|------------|------------|------|
| TTCAGAAAAA | TGATTAATGT | GTTTCAATAA | AATCTCTCCT | TCTTTGTGAA | 50 |
| CATATTCATT | TTTATACTAA | TTAATATAAT | TTCCAAAAAA | GTTTCTGTTT | 100 |
| AAAAGTGAAA | AATATTATTT | ACCGTTTGAC | TTAAATCTTC | AATATATAGG | 150 |
| TGTTTATATG | TATCATTTTG | CGCCAATTTG | AATAAACGGG | AATCAAGTCT | 200 |
| GTTTCTGAGT | TTATTTCAAC | TTTCTTATAG | TAAACATTGT | CTTAATATGA | 250 |
| TGAACTTCAA | TAAAACTTTC | CCTATGCCCC | ATAAAATTTT | CTCAAAATCA | 300 |
| AAAATAACAT | ACCTTACAAC | TTTTACCGTC | GATATCAATT | GCTCTTTTCT | 350 |
| TAATTTAGGA | TTGCTTTCAA | ATTTTGTACT | ATAACGTGAA | ACTACTTTTC | 400 |
| CTTCTTTATA | ATTAAAATTT | ACTAATTCAC | AATCATTTTT | ACTTCCATTT | 450 |
| ACAAAAACAT | CCACTGTTTC | TAACACAAAA | TCTAATAAAC | TTCCTTTAT | 500 |
| TAATCGTAGG | CATTGTATAT | TTCCTTTCAT | TCTTTCCTGA | TTCCATTAGT | 550 |
| TTAAATTTAA | AATTTTCATCC | ATCAATTTCT | TAATTTAATT | GTAGTTCCAT | 600 |
| AATCAATATA | ATTTGTACAG | TTATTATATA | TTCTAGATCA | TCAATAGTTG | 650 |
| AAAAATGGTT | TATTAAACAC | TCTATAAACA | TCGTATGATA | TTGCAAGGTA | 700 |
| TAATCCAATA | TTTCATATAT | GTAATTCCTC | CACATCTCAT | TAAATTTTTA | 750 |
| AATTATACAC | AACCTAATTT | TTAGTTTTAT | TTATGATACG | CTTCTCCACG | 800 |
| CATAATCTTA | AATGCTCTGT | ACACTTG TTC | AATTAACACA | ACCCGCATCA | 850 |
| TTTGATGTGG | GAATGTCATT | TTGCTGAATG | ATAGTGCGTA | GTTACTGCGT | 900 |
| TGTAAGACGT | CCTTGTGCAG | GCCGTTTGAT | CCGCCAATGA | CGAATACAAA | 950 |
| GTCGCTTTGC | CCTTGGGTCA | TGCGTTGGTT | CAATTCTTGG | GCCAATCCTT | 1000 |
| CGGAAGATAG | CATCTTTCCT | TGTATTTCTA | ATGTAATGAC | TGTTGATTGT | 1050 |
| GGTTTGATTT | TGGCTAGTAT | TCGTTGGCCT | TCTTTTTCTT | TTACTTGCTC | 1100 |
| AATTTCTTTG | TCGCTCATAT | TTTCTGGTGC | TTTTTCGTCT | GGAACTTCTA | 1150 |
| TGATGTCTAT | CTTGGTGTAT | GGGCCTAAAC | GTTTTTCATA | TTCTGCTATG | 1200 |
| GCTTGCTTCC | AATATTTCTC | TTTTAGTTTC | CCTACAGCTA | AAATGGTGAT | 1250 |
| TTTCAT | | | | | 1256 |

2) INFORMATION FOR SEQ ID NO: 105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105

TCATGAACCT CATTACTTAT GATAAGIT

28

2) INFORMATION FOR SEQ ID NO: 106

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106

GAAAAAACCG CATCATTTAT GATATGIT

28

2) INFORMATION FOR SEQ ID NO: 107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107

CCTAATTTTT AGTTTTATTT ATGATACGIT

30

2) INFORMATION FOR SEQ ID NO: 108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108

CACAACCTAA TTTTGTAGTTT TATTTATGAT ACGIT

35

2) INFORMATION FOR SEQ ID NO: 109

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109

TGATAAGCCA TTCATTCACC CTAA

24

2) INFORMATION FOR SEQ ID NO: 110

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110

AAGGACTCCT AATTTATGTC TAATTCC

27

2) INFORMATION FOR SEQ ID NO: 111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111

ATGGGAGTCC TTCGCTATTC TGTG

24

2) INFORMATION FOR SEQ ID NO: 112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112

CACTTTTAT TCTTCAAAGA TTTGAGC

27

2) INFORMATION FOR SEQ ID NO: 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113

ATGGAAATTC TTAATCTTTA CTTGTACC

28

2) INFORMATION FOR SEQ ID NO: 114

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114

AGCATCTTCT TTACATCGCT TACT

24

2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115

CAGCAATTCW CATAAACCTC ATA

23

2) INFORMATION FOR SEQ ID NO: 116

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116

ACAAACTTTG AGGGGATTTT TAGTAAA

27

2) INFORMATION FOR SEQ ID NO: 117

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117

TATATTGTGG CATGATTTCT TC

22

2) INFORMATION FOR SEQ ID NO: 118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118

CGAATGGACT AGCACTTTCT AAA

23

2) INFORMATION FOR SEQ ID NO: 119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119

TTGAGGATCA AAAGTTGTTG C

21

2) INFORMATION FOR SEQ ID NO: 120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120

CGATGATTTT ATAGTAGGAG A

21

2) INFORMATION FOR SEQ ID NO: 121

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121

TTCAATCTCT AAATCTAAAT CAGTTTGT

28

2) INFORMATION FOR SEQ ID NO: 122

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122

AGGCGAGAAA ATGGAACATA TCAA

24

2) INFORMATION FOR SEQ ID NO: 123

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123

GGTACAAGTA AAGATTAAGA ATTTCC

26

2) INFORMATION FOR SEQ ID NO: 124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124

AGACAACTTT ATGCAGGTCC TT

22

2) INFORMATION FOR SEQ ID NO: 125

66/125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125

TAACTGCTTG GGTAACCTTA TC

22

2) INFORMATION FOR SEQ ID NO: 126

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126

TATTGCAGGT TTCGATGTTG A

21

2) INFORMATION FOR SEQ ID NO: 127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127

TGACCCATAT CGCCTAAAAT AC

22

2) INFORMATION FOR SEQ ID NO: 128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128

AAAGGACAAC AAGGTAGCAA AG

22

2) INFORMATION FOR SEQ ID NO: 129

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129

TCTGTGGATA AACACCTTGA TG

22

2) INFORMATION FOR SEQ ID NO: 130

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130

GTTTGATCCG CCAATGAC

18

2) INFORMATION FOR SEQ ID NO: 131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131

GGCATAAATG TCAGGAAAAT ATC

23

2) INFORMATION FOR SEQ ID NO: 132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132

GAGGACCAAA CGACATGAAA ATC

23

2) INFORMATION FOR SEQ ID NO: 133

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133

TTCGAGGTTG ATGGGAAGCA

20

2) INFORMATION FOR SEQ ID NO: 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134

CGCTCGACTC AGGGTGTT

18

2) INFORMATION FOR SEQ ID NO: 135

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135

CGTTGAAGAT GCCTTTGA

18

2) INFORMATION FOR SEQ ID NO: 136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136

TTTTGCAACA GCCATTCTG

18

2) INFORMATION FOR SEQ ID NO: 137

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137

GCACACATGT TGTAAGTTTG C

21

2) INFORMATION FOR SEQ ID NO: 138

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138

ACGCAAACCTT ACAACATGTG TG

22

2) INFORMATION FOR SEQ ID NO: 139

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139

CGTTTGTCTG ATTTGGAGGA AG

22

2) INFORMATION FOR SEQ ID NO: 140

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140

TTTCTTCATC ATCGGTCATA AAAT

24

2) INFORMATION FOR SEQ ID NO: 141

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141

CTACGTGAAT CAAAAACAAT GGA

23

2) INFORMATION FOR SEQ ID NO: 142

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142

TACTGCAAAG TCTCGTTCAT CC

22

2) INFORMATION FOR SEQ ID NO: 143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143

CATACCATTT TGAACGATGA CCTC

24

2) INFORMATION FOR SEQ ID NO: 144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144

ATGTCTGGTC AACTTTCCGA CTC

23

2) INFORMATION FOR SEQ ID NO: 145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145

CAATCGGTAT CTGTAAATAT CAAAT

25

2) INFORMATION FOR SEQ ID NO: 146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146

TCGCATACCT GTTTATCTTC TACT

24

2) INFORMATION FOR SEQ ID NO: 147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147

TTGGTTCCAT CTGAACTTTG AG

22

2) INFORMATION FOR SEQ ID NO: 148

73/125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148

AATGGCTTAT CAAAGTGAAT ATGC

24

2) INFORMATION FOR SEQ ID NO: 149

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149

TAATTTTCCTT TTTTCCATT CCTC

24

2) INFORMATION FOR SEQ ID NO: 150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150

ACTAGAATCT CCAAATGAAT CCAGT

25

2) INFORMATION FOR SEQ ID NO: 151

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single

74/125

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151

TGGAGTTAAT CTACGTCTCA TCTC

24

2) INFORMATION FOR SEQ ID NO: 152

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152

G TTCATACAG AAGACTCCTT TTTG

24

2) INFORMATION FOR SEQ ID NO: 153

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153

AGTTTTGATT ATCCGAATAA ATGCT

25

2) INFORMATION FOR SEQ ID NO: 154

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 bases

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154

75/125

TTTAAATTCA GCTATATGGG GAGA

24

2) INFORMATION FOR SEQ ID NO: 155

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155

TTCCGTTTTG CTATTCCATA AT

22

2) INFORMATION FOR SEQ ID NO: 156

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156

CCTCTGATAA AAAACTTGTG AAAT

24

2) INFORMATION FOR SEQ ID NO: 157

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157

ACTACTCCTG GAATTACAAA CTGG

24

2) INFORMATION FOR SEQ ID NO: 158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158

GCCAAAATTA AACCACAATC CAC

23

2) INFORMATION FOR SEQ ID NO: 159

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159

CATTTTGCTG AATGATAGTG CGTA

24

2) INFORMATION FOR SEQ ID NO: 160

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160

CGACCGGATT CCCACATCAA ATGATGCGGG TTGTGTTAAT TCCGGTCG

48

2) INFORMATION FOR SEQ ID NO: 161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid

77/125

- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161

CCCGCGCRTA GTTACTRCGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 162

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162

CCCCGTAGTT ACTGCGTTGT AAGACGGGG

29

2) INFORMATION FOR SEQ ID NO: 163

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163

CCCGCGCATA GTTACTGCGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164

CCCGCGCGTA GTTACTACGT TGTAAGACGT CCGCGGG

37

2) INFORMATION FOR SEQ ID NO: 165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1282 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165

| | | | | | |
|------------|------------|------------|------------|-------------|------|
| ACCATTTTAG | CTGTAGGGAA | ACTAAAAGAG | AAATATTGGA | AGCAAGCCAT | 50 |
| AGCAGAATAT | GAAAAACGTT | TAGGCCCAT | CACCAAGATA | GACATCATAG | 100 |
| AAGTTCCAGA | CGAAAAAGCA | CCAGAAAATA | TGAGCGACAA | AGAAATTGAG | 150 |
| CAAGTAAAAG | AAAAAGAAGG | CCAACGAATA | CTAGCCAAAA | TCAAACCACA | 200 |
| ATCCACAGTC | ATTACATTAG | AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | 250 |
| GATTGGCCCA | AGAATTGAAC | CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | 300 |
| GTATTCGTCA | TTGGCGGATC | AAACGGCCTG | CACAAGGACG | TCTTACAACG | 350 |
| CAGTAACTAT | GCACTATCAT | TTAGCAAAAT | GACATTCCCA | CATCAAATGA | 400 |
| TGCGGGTTGT | GTTAATTGAA | CAAGTGTATA | GAGCATTTAA | GATTATGCGT | 450 |
| GGAGAAGCGT | ACCACAAATA | AAACTAAAAA | ATATGAGAAA | ATTATTAAAT | 500 |
| TAGCTCAAAT | CTTTGAAGAA | TAAAAAGTGA | ATATTAAGTT | TGATAATTTA | 550 |
| GGTACAAGTA | AAGATTAAGA | ATTTCCATTA | TTTAATACAT | GGTGTGTAAA | 600 |
| TCGACTTCTT | TTTGTATTAG | ATGTTTGCAG | TAAGCGATGT | AAAGAAGATG | 650 |
| CTAATAAATA | TGTGAGGAAT | GATTACGATA | CTAGATAAGC | GGCTAATGAA | 700 |
| ATTTTTTAAA | GTACATATAT | AGACATATTT | TTCATTTAGT | AAAATTTTGA | 750 |
| ATTTCACTTT | GCTAAGACTA | GTGTCTAGAA | ATTTATAATG | ATTTATTAAC | 800 |
| ACCTATTTGA | AACTTAAGTA | TAATAAATGA | TTCGGATTTT | ATTTTTTAATA | 850 |
| AAGACAAACT | TGAACGTAGC | AAAGTAGTTT | TTATGATAAA | TAATAAGTTT | 900 |
| TAATAATGTG | ACGCTTTTAT | ATAAGCACAT | TATTATGAAC | AATGTGAATT | 950 |
| GAGCATCTAC | AATTACATTA | ATAAATATAT | AAATGATGAT | TTAAATTCAC | 1000 |
| ATATATTTAT | AATACACATA | CTATATGAAA | GTTTTGATTA | TCCGAATAAA | 1050 |
| TGCTAAAATT | AATAAAATAA | TTAAAGGAAT | CATACTTATT | ATACGTATAC | 1100 |
| GTTTAGCTAC | TGAACTACTG | GATTCATTTG | GAGATTCTAG | TAGTTCTTTT | 1150 |
| TCAATCTCTA | AATCTAAATC | AGTTTTGTAA | TAACCATTAA | TTCTTAATCT | 1200 |
| TTCATCTAGC | TCTGTACTTT | TTTCATCATT | TTTATCTTTG | TTGATATGTT | 1250 |
| CCATTTTCTC | GCCTCTTTTT | AATCAAGTAG | AA | | 1282 |

2) INFORMATION FOR SEQ ID NO: 166

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108 bases
- (B) TYPE: Nucleic acid

79/125

- (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166

| | | | | | |
|------------|------------|------------|------------|------------|------|
| ACCATTTTAG | CTGTAGGGAA | ACTAAAAGAG | AAATATTGGA | AGCAAGCCAT | 50 |
| AGCAGAATAT | GAAAAACGTT | TAGGCCCAT | CACCAAGATA | GACATCATAG | 100 |
| AAGTTCCAGA | CGAAAAAGCA | CCAGAAAATA | TGAGCGACAA | AGAAATTGAG | 150 |
| CAAGTAAAAG | AAAAAGAAGG | CCAACGAATA | CTAGCCAAAA | TCAAACCACA | 200 |
| ATCCACAGTC | ATTACATTAG | AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | 250 |
| GATTGGCCCA | AGAATTGAAC | CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | 300 |
| GTATTCGTCA | TTGGCGGATC | AAACGGCCTG | CACAAGGACG | TCTTACAACG | 350 |
| CAGTAACTAT | GCACTATCAT | TTAGCAAAAT | GACATTCCCA | CATCAAATGA | 400 |
| TGCGGGTTGT | GTTAATTGAA | CAAGTGTATA | GAGCATTTAA | GATTATGCGT | 450 |
| GGAGAAGCGT | ACCACAAATA | AAACTAAAAA | ATATGAGAAA | ATTATTAAAT | 500 |
| TAGCTCAAAT | CTTTGAAGAA | TAAAAAGTGA | ATATTAAGTT | TGATAATTTA | 550 |
| GGTACAAGTA | AAGATTAAGA | ATTTCCATTA | TTTAATACAT | GGTGTGTAAA | 600 |
| TCGACTTCTT | TTTGTATTAG | ATGTTTGCAG | TAAGCGATGT | AAAGAAGATG | 650 |
| CTAATAAATA | TGTGAGGAAT | GATTACGATA | CTAGATAAGC | GGCTAATGAA | 700 |
| ATTTTTTAAA | GTACATATAT | AGACATATTT | TTCATTTAGT | AAAATTTTGA | 750 |
| ATTTCACTTT | GCTAAGACTA | GTGTCTAGAA | ATTTATAATG | ATTTATTAAC | 800 |
| ACCTATTTGA | AACTTAAGTA | TAATAAATGA | TTCGGATTTT | ATTTTTAATA | 850 |
| AAGACAAACT | TGAACGTAGC | AAAGTAGTTT | TTATGATAAA | TAATAAGTTT | 900 |
| TAATAATGTG | ACGCTTTTAT | ATAAGCACAT | TATTATGAAC | AATGTGAATT | 950 |
| GAGCATCTAC | AATTACATTA | ATAAATATAT | AAATGATGAT | TTAAATTCAC | 1000 |
| ATATATTTAT | AATACACATA | CTATATGAAA | GTTTTGATTA | TCCGAATAAA | 1050 |
| TGCTAAAATT | AATAAAATAA | TTAAAGGAAT | CATACTTATT | ATACGTATAC | 1100 |
| GTTTAGCT | | | | | 1108 |

2) INFORMATION FOR SEQ ID NO: 167

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1530 bases
(B) TYPE: Nucleic acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
(B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TTAGCTGTAG | GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | CCATAGCAGA | 50 |
| ATATGAAAAA | CGTTTAGGCC | CATACACCAA | GATAGACATC | ATAGAAGTTC | 100 |

| | | | | | |
|-------------|-------------|-------------|-------------|-------------|------|
| CAGACGAAAA | AGCACCAGAA | AATATGAGCG | ACAAAGAAAT | TGAGCAAGTA | 150 |
| AAAGAAAAAG | AAGGCCAACG | AATACTAGCC | AAAATCAAAC | CACAATCCAC | 200 |
| AGTCATTACA | TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | GAAGGATTGG | 250 |
| CCCAAGAATT | GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | CTTTGTATTC | 300 |
| GTCATTGGCG | GATCAAACGG | CCTGCACAAG | GACGTCTTAC | AACGCAGTAA | 350 |
| CTATGCACTA | TCATTTAGCA | AAATGACATT | CCCACATCAA | ATGATGCGGG | 400 |
| TTGTGTTAAT | TGAACAAGTG | TATAGAGCAT | TTAAGATTAT | GCGTGGAGAA | 450 |
| GCATATCATA | AATGATGCGG | TTTTTTTCAGC | CGCTTCATAA | AGGGGGGTGA | 500 |
| TCATATCGGA | ACGTATGAGG | TTTATGAGAA | TTGCTGCTAT | GTTTTTTATGA | 550 |
| AGCGTATCAT | AAATGATGCA | GTTTTTTGATA | ATTTTTTCTT | TATCAGAGAT | 600 |
| TTTACTAAAA | ATCCCCTCAA | AGTTTGTTTT | TTTCAACTTC | AACTTTGAAG | 650 |
| GGAATAAATA | AGGAACTTAT | TTATATTTAT | CCTTTATCTC | ATTAATATCT | 700 |
| ATTTTTTTTAT | TAATAATATT | ATAAATATTA | AATTCTTTAG | AAAAGTCACT | 750 |
| ATCACTCTTA | TTCTTCATAC | TAAACGTTAT | TAATCTAATA | ATATCAGCTA | 800 |
| CTATTTCTTT | AAATTCTATT | GCATCTTCTT | TTTTATAAGT | AGCGCCTGTA | 850 |
| TGAACAATTT | TATTTCTCAT | ACCATAGTAA | TCTTTCATAT | ATTTTTTTTAC | 900 |
| ACAATTTTTA | ATTTCAATTAG | AATTATCCAA | ATCTAGATTA | TCAATTGTCT | 950 |
| TTAATAAATG | ATCATTAACA | ACATTAGCAT | ACCCACATCC | AAGCTTCTTT | 1000 |
| TTTATCTCTT | CATCACTTAA | ATTTTCATCT | AATTTATAAT | ATCTTTCTAA | 1050 |
| AAAATTTGTG | ATAAAAACCTT | CTAATGCAGT | CTGAATTTGT | ACAATTGCTA | 1100 |
| AATTATAGTC | AGATTTATAA | AAAGAACGTT | CACCTTTTCT | CATAGCCAAA | 1150 |
| ACATAAATAT | TGCTAGGATG | ATTATTGAAA | ATATTATAAT | TTTTTTTAAAT | 1200 |
| ATTTAATAAA | TCACTTTTTT | TGATAGATGA | ATACTGATCT | TCTTCTATCT | 1250 |
| TTCCAGGCAT | GTCAATCATG | AAAATACTCA | TCTCTTTTAT | ATTTCCATCT | 1300 |
| ATAGTATATA | TTATATAATA | TGGAATACTT | AATATATCCC | CTAATGATAG | 1350 |
| CTGGTATATA | TTATGATACT | GATATTTAAC | GCTAATAATT | TTAATAAGAT | 1400 |
| TATTTAGACA | ATTAAATTGC | TTATTAAAAA | TTTTTCGTTAG | ACTATTACTT | 1450 |
| TTCTTTGATT | CCCTAGAAGT | AGAATTTGAT | TTCAATTTTT | TAAACTGATT | 1500 |
| GTGCTTGATT | ATTGAAGTTA | TTTCAACATA | | | 1530 |

2) INFORMATION FOR SEQ ID NO: 168

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1256 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GCTGTAGGGA | AACTAAAAGA | GAAATATTGG | AAGCAAGCCA | TAGCAGAATA | 50 |
| TGAAAAACGT | TTAGGCCCAT | ACACCAAGAT | AGACATCATA | GAAGTTCCAG | 100 |
| ACGAAAAAGC | ACCAGAAAAT | ATGAGCGACA | AAGAAATTGA | GCAAGTAAAA | 150 |
| GAAAAAGAAG | GCCAACGAAT | ACTAGCCAAA | ATTAAACCAC | AATCCACAGT | 200 |
| CATTACATTA | GAAATACAAG | GAAAGATGCT | ATCTTCCGAA | GGATTGGCCC | 250 |
| AAGAATTGAA | CCAACGCATG | ACCCAAGGGC | AAAGCGACTT | TGTATTGCTC | 300 |
| ATTGGCGGAT | CAAACGGCCT | GCACAAGGAC | GTCTTACAAC | GCAGTAACTA | 350 |
| CGCACTATCA | TTCAGCAAAA | TGACATTCCC | ACATCAAATG | ATGCGGGTTG | 400 |
| TGTTAATTGA | GCAAGTGTAT | AGAGCATTTA | AGATTATGCG | TGGAGAAGCA | 450 |

| | | | | | |
|--------------|------------|------------|------------|------------|------|
| TATCATAAAT | GATGCGGTTT | TTTCAGCCGC | TTCATAAAGG | GATTTTGAAT | 500 |
| GTATCAGAAC | ATATGAGGTT | TATGTGAATT | GCTGTTATGT | TTTTAAGAAG | 550 |
| CATATCATAA | GTGATGCGGT | TTTTATTAAT | TAGTTGCTAA | AAAATGAAGT | 600 |
| ATGCAATATT | AATTATTATT | AAATTTTGAT | ATATTTAAAG | AAAGATTAAG | 650 |
| TTTAGGGTGA | ATGAATGGCT | TATCAAAGTG | AATATGCATT | AGAAAATGAA | 700 |
| GTA CT TCAAC | AACTTGAGGA | ATTGAACTAT | GAAAGAGTAA | ATATACATAA | 750 |
| TATTAAATTA | GAAATTAATG | AATATCTCAA | AGAACTAGGA | GTGTTGAAAA | 800 |
| ATGAATAAGC | AGACAAATAC | TCCAGAACTA | AGATTTCCAG | AGTTTGATGA | 850 |
| GGAATGGAAA | AAAAGGAAAT | TAGGTGAAGT | AGTAAATTAT | AAAAATGGTG | 900 |
| GTTCA TTTGA | AAGTTTAGTG | AAAAACCATG | GTGTATATAA | ACTCATAACT | 950 |
| CTTAAATCTG | TTAATACAGA | AGGAAAGTTG | TGTAATTCTG | GAAAATATAT | 1000 |
| CGATGATAAA | TGTGTTGAAA | CATTGTGTAA | TGATACTTTA | GTAATGATAC | 1050 |
| TGAGCGAGCA | AGCACCAGGA | CTAGTTGGAA | TGACTGCAAT | TATACCTAAT | 1100 |
| AATAATGAGT | ATGTACTAAA | TCAACGAGTA | GCAGCACTAG | TGCCTAAACA | 1150 |
| ATTTATAGAT | AGTCAATTTT | TATCTAAGTT | AATTAATAGA | AACCAGAAAT | 1200 |
| ATTTCA GTGT | GAGATCTGCT | GGAACAAAAG | TGAAAAATAT | TTCTAAAGGA | 1250 |
| CATGTA | | | | | 1256 |

2) INFORMATION FOR SEQ ID NO: 169

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| TTACATTAGA | AATACAAGGA | AAGATGCTAT | CTTCCGAAGG | ATTGGCCCAA | 50 |
| GAATTGAACC | AACGCATGAC | CCAAGGGCAA | AGCGACTTTG | TTTTCGTCAT | 100 |
| TGGCGGATCA | AACGGCCTGC | ACAAGGACGT | CTTACAACGC | AGTAACTACG | 150 |
| CACTATCATT | CAGCAAAATG | ACATTCCCAC | ATCAAATGAT | GCGGGTTGTG | 200 |
| TTAATTGAAC | AAGTGTACAG | AGCATTTAAG | ATTATGCGAG | GAGAAGCTTA | 250 |
| TCATAAGTAA | TGAGGTTTCAT | GATTTTTGAC | ATAGTTAGCC | TCCGCAGTCT | 300 |
| TTCATTTCAA | GTAAATAATA | GCGAAATATT | CTTTATACTG | AATACTTATA | 350 |
| GTGAAGCAAA | GTTCTAGCTT | TGAGAAAATT | CTTTCTGCAA | CTAAATATAG | 400 |
| TAAATTACGG | TAAAATATAA | ATAAGTACAT | ATTGAAGAAA | ATGAGACATA | 450 |
| ATATATTTTA | TAATAGGAGG | GAATTTCAAA | TGATAGACAA | CTTTATGCAG | 500 |
| GTCCTTAAAT | TAATTAAAGA | GAAACGTACC | AATAATGTAG | TTAAAAAATC | 550 |
| TGATTGGGAT | AAAGGTGATC | TATATAAAAC | TTTAGTCCAT | GATAAGTTAC | 600 |
| CCAAGCAGTT | AAAAGTGCAT | ATAAAAGAAG | ATAAATATTC | AGTTGTAGGG | 650 |
| AAGGTTGCTA | CTGGGA ACTA | TAGTAAAGTT | CCTTGGATTT | CAATATATGA | 700 |
| TGAGAATATA | ACAAAAGAAA | CAAAGGATGG | ATATTATTTG | GTATATCTTT | 750 |
| TTCATCCGGA | AGGAGAAGGC | ATATACTTAT | CTTTGAATCA | AGGATGGTCA | 800 |
| AAGATAAGTG | ATATGTTTCC | GCGGGATAAA | AATGCTGCAA | AACAAA | 846 |

2) INFORMATION FOR SEQ ID NO: 170

82/125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1270 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170

| | | | | | |
|------------|-------------|-------------|------------|------------|------|
| CATTAGAAAT | ACAAGGAAAG | ATGCTATCTT | CCGAAGGATT | GGCCCAAGAA | 50 |
| TTGAACCAAC | GCATGACCCA | AGGGCAAAGC | GACTTTGTAT | TCGTCATTGG | 100 |
| CGGATCAAAC | GGCCTGCACA | AGGACGTCTT | ACAACGCAGT | AACTATGCAC | 150 |
| TATCATTTAG | CAAAATGACA | TTCCCACATC | AAATGATGCG | GGTTGTGTTA | 200 |
| ATTGAACAAG | TGTATAGAGC | ATTTAAGATT | ATGCGTGGAG | AAGCATATCA | 250 |
| TAAATGATGC | GGTTTTTTCA | GCCGCTTCAT | AAAGGGATTT | TGAATGTATC | 300 |
| AGAACATATG | AGGTTTATGT | GAATTGCTGT | TATGTTTTTA | AGAAGCTTAT | 350 |
| CATAAGTAAT | GAGGTTTCATG | ATTTTTTGACA | TAGTTAGCCT | CCGCAGTCTT | 400 |
| TCATTTCAAG | TAAATAATAG | CGAAATATTC | TTTATACTGA | ATACTTATAG | 450 |
| TGAAGCAAAG | TTCTAGCTTT | GAGAAAATTC | TTTCTGCAAC | TAAATATAGT | 500 |
| AAATTACGGT | AAAATATAAA | TAAGTACATA | TTGAAGAAAA | TGAGACATAA | 550 |
| TATATTTTAT | AATAGGAGGG | AATTTCAAAT | GATAGACAAC | TTTATGCAGG | 600 |
| TCCTTAAATT | AATTAAAGAG | AAACGTACCA | ATAATGTAGT | TAAAAAATCT | 650 |
| GATTGGGATA | AAGGTGATCT | ATATAAAACT | TTAGTCCATG | ATAAGTTACC | 700 |
| CAAGCAGTTA | AAAGTGCATA | TAAAAGAAGA | TAAATATTCA | GTTGTAGGGA | 750 |
| AGGTTGCTAC | TGGGAACTAT | AGTAAAGTTC | CTTGGATTTC | AATATATGAT | 800 |
| GAGAATATAA | CAAAAGAAAC | AAAGGATGGA | TATTATTTGG | TATATCTTTT | 850 |
| TCATCCGGAA | GGAGAAGGCA | TATACTTATC | TTTGAATCAA | GGATGGTCAA | 900 |
| AGATAAGTGA | TATGTTTCCG | CGGGATAAAA | ATGCTGCAAA | ACAAAGAGCA | 950 |
| TTAACTTTAT | CTTCCGAAC | CAATAAATAT | ATTACATCAA | ATGAATTTAA | 1000 |
| TACTGGAAGA | TTTTATTACG | CAGAAAATAA | AGATTCATCT | TATGATTTAA | 1050 |
| AAAATGATTA | TCCATCAGGA | TATTCTCATG | GATCAATAAG | ATTCAAATAT | 1100 |
| TATGATTTGA | ATGAAGGATT | CACAGAAGAA | GATATGCTAG | AGGATTTAAA | 1150 |
| GAAATTTTAA | GAACATTTTA | ATGAATTAGC | TTCAAAAGTT | ACAAAAACAT | 1200 |
| CCTATGATAG | CTTGGTCAAT | AGCATAGACG | AAATACAGGA | AGACAGCGAA | 1250 |
| ATTGAAGAAA | TTAGAACAGC | | | | 1270 |

2) INFORMATION FOR SEQ ID NO: 171

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-9208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171

| | | | | | |
|------------|------------|-------------|------------|-------------|-----|
| ACCATTTTAG | CTGTAGGGAA | ACTAAAAGAG | AAATACTGGA | AGCAAGCCAT | 50 |
| AGCAGAATAT | GAAAAACGTT | TAGGCCCCATA | CACCAAGATA | GACATCATAG | 100 |
| AAGTTCCAGA | CGAAAAAGCA | CCAGAAAATA | TGAACTACAA | AGAAATTGAG | 150 |
| CAAGTAAAAG | AAAAAGAAGG | CCAACGAATA | CTAGCCAAAA | TCAAACCACA | 200 |
| ATCAACAGTC | ATTACATTAG | AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | 250 |
| GATTGGCCCA | AGAATTGAAC | CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | 300 |
| GTATTCGTCA | TTGGCGGATC | AAACGGCCTG | CACAAGGACG | TCTTACAACG | 350 |
| CAGTAACTAC | GCACTATCAT | TCAGCAAAAT | GACATTCCCA | CATCAAATGA | 400 |
| TGCGGGTTGT | GTTAATTGAA | CAAGTGTACA | GAGCATTTAA | GATTATGCGA | 450 |
| GGAGAAGCGT | ATCATAAGTG | ATGGTAAAAA | ATATGAGTAA | GTAGATGAAG | 500 |
| AGTGAAAATC | AGATTAATTA | ATAATAATGT | ATCAAATTTA | AATAAAGGGG | 550 |
| TTTTTAAGTA | TGAATTTAAG | AGGTCATGAA | AATAGACTTA | AATTTTCATGC | 600 |
| GAAATATGAT | GTGACACCTA | TATCACATTT | AAAATTATTA | GAAGGTCAAA | 650 |
| AGAAAGACGG | TGAAGGCGGC | ATACTGACAG | ATAGCTATTA | CTGTTTTTCA | 700 |
| TACAGCTTAA | AAGGTAATTC | TAAAAAAGTT | TTAGGTACGT | TTAATTGTGG | 750 |
| TTATCATATT | GCTGAAGATT | TACTAAAATT | ATCAAATCAA | GATAAATTAC | 800 |
| CTTTATTTAA | CCCGTTTAAA | GTAATTAATG | AAGGTAATCA | ATTGCAGGGC | 850 |
| GTAACGAATA | AAGGTAATTT | AAATATTAAT | AGGCAAAGAA | AACAGTATAA | 900 |
| TGAAGTGGCT | TTACAGCTTT | CAAATGCTAT | TAATTTAATC | ATAATTTGTT | 950 |
| ATGAGGATAA | TATTAAAGAA | CCACTTTCAA | CGATAAAATA | C | 991 |

2) INFORMATION FOR SEQ ID NO: 172

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 748 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-9770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATCGTTTAAC | GTGTCACATG | ATGCGATAGA | TCCGCAATTT | TATATTTTCC | 50 |
| ATAATAACTA | TAAGAAGTTT | ACGATTTTAA | CAGATACGGG | TTACGTGTCT | 100 |
| GATCGTATGA | AAGGTATGAT | ACGTGGCAGC | GATGCATTTA | TTTTTGAGAG | 150 |
| TAATCATGAC | GTCGATATGT | TGAGAATGTG | TCGTTATCCA | TGGAAGACGA | 200 |
| AACAACGCAT | TTTAGGCGAT | ATGGGTCATG | TATCTAATGA | GGATGCGGGT | 250 |
| CATGCGATGA | CAGACGTGAT | TACAGGTAAC | ACGAAACGTA | TTTACTTATC | 300 |
| GCATTTATCA | CAAGATAATA | ATATGAAAGA | TTTGGCGCGT | ATGAGTGTG | 350 |
| GCCAAGTATT | GAACGAACAC | GATATTGATA | CGGAAAAAGA | AGTATTGCTA | 400 |
| TGTGATACGG | ATAAAGCTAT | TCCAACACCA | ATATATACAA | TATAAATGAG | 450 |
| AGTCATCCGA | TAAAGTTCCG | CACTGCTGTG | AAACGACTTT | ATCGGGTGCT | 500 |
| TTTTTATGTT | GTTGGTGGGA | AATGGCTGTT | GTTGAGTTGA | ATCGGATTGA | 550 |
| TTGAAATGTG | TAAAATAATT | CGATATTAAA | TGTAATTTAT | AAATAATTTA | 600 |

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CATAAAATCA | AACATTTTAA | TATAAGGATT | ATGATAATAT | ATTGGTGTAT | 650 |
| GACAGTTAAT | GGAGGGAACG | AAATGAAAGC | TTTATTACTT | AAAACAAGTG | 700 |
| TATGGCTCGT | TTTGCTTTTT | AGTGTGATGG | GATTATGGCA | TGTCTCGA | 748 |

2) INFORMATION FOR SEQ ID NO: 173

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 917 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173

| | | | | | |
|-------------|------------|-------------|------------|------------|-----|
| AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | GATTGGCCCA | AGAATTGAAC | 50 |
| CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | GTATTCGTCA | TTGGCGGATC | 100 |
| AAACGGCCTG | CACAAGGACG | TCTTACAACG | TAGTAACTAC | GCACTATCAT | 150 |
| TCAGCAAAAT | GACATTCCCA | CATCAAATGA | TGCGGGTTGT | GTTAATTGAG | 200 |
| CAAGTGTATA | GAGCATTTAA | GATTATGCGT | GGAGAAGCAT | ATCATAAATG | 250 |
| ATGCGGTTTT | TTCAGCCGCT | TCATAAAGGG | ATTTTGAATG | TATCAGAACA | 300 |
| TATGAGGTTT | ATGTGAATTG | CTGTTATGTT | TTTAAGAAGC | TTATCATAAG | 350 |
| TAATGAGGTT | CATGATTTTT | GACATAGTTA | GCCTCCGCAG | TCTTTCATTT | 400 |
| CAAGTAAATA | ATAGCGAAAT | ATTCTTTTATA | CTGAATACTT | ATAGTGAAGC | 450 |
| AAAGTTCCTAG | CTTTGAGAAA | ATTCTTTCTG | CAACTAAATA | TAGTAAATTA | 500 |
| CGGTAAAATA | TAAATAAGTA | CATATTGAAG | AAAATGAGAC | ATAATATATT | 550 |
| TTATAATAGG | AGGGAATTTT | AAATGATAGA | CAACTTTATG | CAGGTCCTTA | 600 |
| AATTAATTAA | AGAGAAACGT | ACCAATAATG | TAGTTAAAAA | ATCTGATTGG | 650 |
| GATAAAGGTG | ATCTATATAA | AACTTTAGTC | CATGATAAGT | TACCCAAGCA | 700 |
| GTTAAAAGTG | CATATAAAAG | AAGATAAATA | TTCAGTTGTA | GGGAAGGTTG | 750 |
| CTACTGGGAA | CTATAGTAAA | GTTCTTGGA | TTTCAATATA | TGATGAGAAT | 800 |
| ATAACAAAAG | AAACAAAGGA | TGGATATTAT | TTGGTATATC | TTTTTCATCC | 850 |
| GGAAGGAGAA | GGCATATACT | TATCTTTGAA | TCAAGGATGG | TCAAAGATAA | 900 |
| GTGATATGTT | TCCGCGG | | | | 917 |

2) INFORMATION FOR SEQ ID NO: 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1132 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-9865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174

| | | | | | |
|-------------|------------|------------|------------|-------------|------|
| GCTGTAGGGA | AACTAAAAGA | GAAATATTGG | AAGCAAGCCA | TAGCAGAATA | 50 |
| TGAAAAACGT | TTAGGCCCAT | ACACCAAGAT | AGACATCATA | GAAGTTCCAG | 100 |
| ACGAAAAAGC | ACCAGAAAAT | ATGAGCGACA | AAGAAATTGA | GCAAGTAAAA | 150 |
| GAAAAAGAAG | GCCAACGAAT | ACTAGCCAAA | ATCAAACCAC | AATCAACAGT | 200 |
| CATTACATTA | GAAATACAAG | GAAAGATGCT | ATCTTCCGAA | GGATTGGCCC | 250 |
| AAGAATTGAA | CCAACGCATG | ACCCAAGGGC | AAAGCGACTT | TGTATTTCGTC | 300 |
| ATTGGCGGAT | CAAACGGCCT | GCACAAGGAC | GTCTTACAAC | GTAGTAACTA | 350 |
| CGCACTATCA | TTCAGCAAAA | TGACATTCCC | ACATCAAATG | ATGCGGGTTG | 400 |
| TGTTAATTGA | GCAAGTGTAT | AGAGCATTTA | AGATTATGCG | TGGAGAAGCA | 450 |
| TATCATAAAT | GATGCGGTTT | TTTCAGCCGC | TTCATAAAGG | GATTTTGAAT | 500 |
| GTATCAGAAC | ATATGAGGTT | TATGTGAATT | GCTGTTATGT | TTTTAAGAAG | 550 |
| CTTATCATAA | GTAATGAGGT | TCATGATTTT | TGACATAGTT | AGCCTCCGCA | 600 |
| GTCTTTCATT | TCAAGTAAAT | AATAGCGAAA | TATTCTTTAT | ACTGAATACT | 650 |
| TATAGTGAAG | CAAAGTTCTA | GCTTTGAGAA | AATTCTTTCT | GCAACTAAAT | 700 |
| ATAGTAAATT | ACGGTAAAAT | ATAAATAAGT | ACATATTGAA | GAAAATGAGA | 750 |
| CATAATATAT | TTTATAATAG | GAGGGAATTT | CAAATGATAG | ACAAC TTTAT | 800 |
| GCAGGTCCTT | AAATTAATTA | AAGAGAAACG | TACCAATAAT | GTAGTTAAAA | 850 |
| AATCTGATTG | GGATAAAGGT | GATCTATATA | AAACTTTAGT | CCATGATAAG | 900 |
| TTACCCAAGC | AGTTAAAAGT | GCATATAAAA | GAAGATAAAT | ATTCAGTTGT | 950 |
| AGGGAAGGTT | GCTACTGGGA | ACTATAGTAA | AGTTCCTTGG | ATTTCAATAT | 1000 |
| ATGATGAGAA | TATAACAAAA | GAAACAAAGG | ATGGATATTA | TTTGGTATAT | 1050 |
| CTTTTTTCATC | CGGAAGGAGA | AGGCATATAC | TTATCTTTGA | ATCAAGGATG | 1100 |
| GTCAAAGATA | AGTGATATGT | TTCCGCGGGA | TA | | 1132 |

2) INFORMATION FOR SEQ ID NO: 175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: CCRI-9866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175

| | | | | | |
|------------|------------|------------|------------|-------------|-----|
| AGCTGTAGGG | AACTAAAAG | AGAAATATTG | GAAGCAAGCC | ATAGCAGAAT | 50 |
| ATGAAAAACG | TTTAGGCCCA | TACACCAAGA | TAGACATCAT | AGAAGTTCCA | 100 |
| GACGAAAAAG | CACCAGAAAA | TATGAGCGAC | AAAGAAATTG | AGCAAGTAAA | 150 |
| AGAAAAAGAA | GGCCAACGAA | TACTAGCCAA | AATCAAACCA | CAATCAACAG | 200 |
| TCATTACATT | AGAAATACAA | GGAAAGATGC | TATCTTCCGA | AGGATTGGCC | 250 |
| CAAGAATTGA | ACCAACGCAT | GACCCAAGGG | CAAAGCGACT | TTGTATTTCGT | 300 |
| CATTGGCGGA | TCAAACGGCC | TGCACAAGGA | CGTCTTACAA | CGTAGTAACT | 350 |
| ACGCACTATC | ATTGAGCAAA | ATGACATTCC | CACATCAAAT | GATGCGGGTT | 400 |
| GTGTTAATTG | AGCAAGTGTA | TAGAGCATTT | AAGATTATGC | GTGGAGAAGC | 450 |

| | | | | | |
|-------------|------------|-------------|-------------|------------|------|
| ATATCATAAA | TGATGCGGTT | TTTTTCAGCCG | CTTCATAAAG | GGATTTTGAA | 500 |
| TGTATCAGAA | CATATGAGGT | TTATGTGAAT | TGCTGTTATG | TTTTTAAGAA | 550 |
| GCTTATCATA | AGTAATGAGG | TTCATGATTT | TTGACATAGT | TAGCCTCCGC | 600 |
| AGTCTTTCAT | TTCAAGTAAA | TAATAGCGAA | ATATTCTTTA | TACTGAATAC | 650 |
| TTATAGTGAA | GCAAAGTTCT | AGCTTTGAGA | AAATTCTTTC | TGCAACTAAA | 700 |
| TATAGTAAAT | TACGGTAAAA | TATAAATAAG | TACATATTGA | AGAAAATGAG | 750 |
| ACATAATATA | TTTTATAATA | GGAGGGAATT | TCAAATGATA | GACAACTTTA | 800 |
| TGCAGGTCCT | TAAATTAATT | AAAGAGAAAC | GTACCAATAA | TGTAGTTAAA | 850 |
| AAATCTGATT | GGGATAAAGG | TGATCTATAT | AAAACCTTTAG | TCCATGATAA | 900 |
| GTTACCCAAG | CAGTTAAAAG | TGCATATAAA | AGAAGATAAA | TATTCAGTTG | 950 |
| TAGGGAAGGT | TGCTACTGGG | AACTATAGTA | AAGTTCCTTG | GATTTCAATA | 1000 |
| TATGATGAGA | ATATAACAAA | AGAAACAAAG | GATGGATATT | ATTTGGTATA | 1050 |
| TCTTTTTTCAT | CCGGAAGGAG | AAGGCATATA | CTTATCTTTG | AATCAAGGAT | 1100 |
| GGTCAAAGAT | AAGTGATATG | TTTCCGCGGG | ATA | | 1133 |

2) INFORMATION FOR SEQ ID NO: 176

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1087 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| ACTAAAAGAG | AAATATTGGA | AGCAAGCCAT | AGCAGAATAT | GAAAAACGTT | 50 |
| TAGGCCCAT | CACCAAGATA | GACATCATAG | AAGTTCCAGA | CGAAAAAGCA | 100 |
| CCAGAAAATA | TGAGCGACAA | AGAAATTGAG | CAAGTAAAAG | AAAAAGAAGG | 150 |
| CCAACGAATA | CTAGCCAAAA | TCAAACCACA | ATCAACAGTC | ATTACATTAG | 200 |
| AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | GATTGGCACA | AGAATTGAAC | 250 |
| CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | GTATTCGTCA | TTGGCGGATC | 300 |
| AAACGGCCTG | CACAAGGACG | TCTTACAACG | TAGTAACTAC | GCACTATCAT | 350 |
| TCAGCAAAAT | GACATTCCCA | CATCAAATGA | TGCGGGTTGT | GTTAATTGAG | 400 |
| CAAGTGTATA | GAGCGTTTAA | GATTATGCGT | GGAGAAGCAT | ATCATAAATG | 450 |
| ATGCGGTTTT | TTCAGCCGCT | TCATAAAGGG | ATTTTGAATG | TATCAGAACA | 500 |
| TATGAGGTTT | ATGTGAATTG | CTGTTATGTT | TTTAAGAAGC | TTATCATAAG | 550 |
| TAATGAGGTT | CATGATTTTT | GACATAGTTA | GCCTCCGCAG | TCTTTCATTT | 600 |
| CAAGTAAATA | ATAGCGAAAT | ATTCTTTTATA | CTGAATACTT | ATAGTGAAGC | 650 |
| AAAGTTCTAG | CTTTGAGAAA | ATTCTTTCTG | CAACTAAATA | TAGTAAATTA | 700 |
| CGGTAAAATA | TAAATAAGTA | CATATTGAAG | AAAATGAGAC | ATAATATATT | 750 |
| TTATAATAGG | AGGGAATTTT | AAATGATAGA | CAACTTTATG | CAGGTCCTTA | 800 |
| AATTAATTAA | AGAGAAACGT | ACCAATAATG | TAGTTAAAAA | ATCTGATTGG | 850 |
| GATAAAGGTG | ATCTATATAA | AACTTTAGTC | CATGATAAGT | TACCCAAGCA | 900 |
| GTTAAAAGTG | CATATAAAAG | AAGATAAATA | TTCAGTTGTA | GGGAAGGTTG | 950 |
| CTACTGGGAA | CTATAGTAAA | GTTCTTTGGA | TTTCAATATA | TGATGAGAAT | 1000 |
| ATAACAAAAG | AAACAAAGGA | TGGATATTAT | TTGGTATATC | TTTTTCATCC | 1050 |
| GGAAGGAGAA | GGCATATACT | TATCTTTGAA | TCAAGGA | | 1087 |

2) INFORMATION FOR SEQ ID NO: 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 903 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177

| | | | | | |
|-------------|------------|-------------|------------|------------|-----|
| CAAGGAAAGA | TGCTATCTTC | CGAAGGATTG | GCCCAAGAAT | TGAACCAACG | 50 |
| CATGACCCAA | GGGCAAAGCG | ACTTTGTATT | CGTCATTGGC | GGATCAAACG | 100 |
| GCCTGCACAA | GGACGTCTTA | CAACGTAGTA | ACTACGCACT | ATCATTCAGC | 150 |
| AAAATGACAT | TCCCACATCA | AATGATGCGG | GTTGTGTTAA | TTGAGCAAGT | 200 |
| GTATAGAGCA | TTTAAGATTA | TGCGTGGAGA | AGCATATCAT | AAATGATGCG | 250 |
| GTTTTTTCAG | CCGCTTCATA | AAGGGATTTT | GAATGTATCA | GAACATATGA | 300 |
| GGTTTATGTG | AATTGCTGTT | ATGTTTTTAA | GAAGCTTATC | ATAAGTAATG | 350 |
| AGGTTTCATGA | TTTTTGACAT | AGTTAGCCTC | CGCAGTCTTT | CATTTCAGT | 400 |
| AAATAATAGC | GAAATATTCT | TTATACTGAA | TACTTATAGT | GAAGCAAAGT | 450 |
| TCTAGCTTTG | AGAAAATTCT | TTCTGCAACT | AAATATAGTA | AATTACGGTA | 500 |
| AAATATAAAT | AAGTACATAT | TGAAGAAAAT | GAGACATAAT | ATATTTTATA | 550 |
| ATAGGAGGGA | ATTTCAAATG | ATAGACAACT | TTATGCAGGT | CCTTAAATTA | 600 |
| ATTAAAGAGA | AACGTACCAA | TAATGTAGTT | AAAAAATCTG | ATTGGGATAA | 650 |
| AGGTGATCTA | TATAAAACTT | TAGTCCATGA | TAAGTTACCC | AAGCAGTTAA | 700 |
| AAGTGCATAT | AAAAGAAGAT | AAATATTTCAG | TTGTAGGGAA | GGTTGCTACT | 750 |
| GGGAACTATA | GTAAAGTTCC | TTGGATTTC | ATATATGATG | AGAATATAAC | 800 |
| AAAAGAAACA | AAGGATGGAT | ATTATTTGGT | ATATCTTTTT | CATCCGGAAG | 850 |
| GAGAAGGCAT | ATACTTATCT | TTGAATCAAG | GATGGTCAAA | GATAAGTGAT | 900 |
| ATG | | | | | 903 |

2) INFORMATION FOR SEQ ID NO: 178

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1114 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178

88/125

| | | | | | |
|-------------|------------|------------|------------|------------|------|
| GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | CCATAGCAGA | ATATGAAAAA | 50 |
| CGTTTAGGCC | CATACACCAA | GATAGACATC | ATAGAAGTTC | CAGACGAAAA | 100 |
| AGCACCAGAA | AATATGAGCG | ACAAAGAAAT | TGAGCAAGTA | AAAGAAAAAG | 150 |
| AAGGCCAACG | AATACTAGCC | AAAATCAAAC | CACAATCAAC | AGTCATTACA | 200 |
| TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | GAAGGATTGG | CCCAAGAATT | 250 |
| GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | CTTTGTATTC | GTCATTGGCG | 300 |
| GATCAAACGG | CCTGCACAAG | GACGTCTTAC | AACGTAGTAA | CTACGCACTA | 350 |
| TCATTTCAGCA | AAATGACATT | CCCACATCAA | ATGATGCGGG | TTGTGTTAAT | 400 |
| TGAGCAAGTG | TATAGAGCAT | TTAAGATTAT | GCGTGGAGAA | GCATATCATA | 450 |
| AATGATGCGG | TTTTTTCAGC | CGCTTCATAA | AGGGATTTTG | AATGTATCAG | 500 |
| AACATATGAG | GTTTATGTGA | ATTGCTGTTA | TGTTTTTAAG | AAGCTTATCA | 550 |
| TAAGTAATGA | GGTTCATGAT | TTTTGACATA | GTTAGCCTCC | GCAGTCTTTC | 600 |
| ATTTCAAGTA | AATAATAGCG | AAATATTCTT | TATACTGAAT | ACTTATAGTG | 650 |
| AAGCAAAGTT | CTAGCTTTGA | GAAAATTCTT | TCTGCAACTA | AATATAGTAA | 700 |
| ATTACGGTAA | AATATAAATA | AGTACATATT | GAAGAAAATG | AGACATAATA | 750 |
| TATTTTATAA | TAGGAGGGAA | TTTCAAATGA | TAGACAACTT | TATGCAGGTC | 800 |
| CTTAAATTAA | TTAAAGAGAA | ACGTACCAAT | AATGTAGTTA | AAAAATCTGA | 850 |
| TTGGGATAAA | GGTGATCTAT | ATAAACTTTT | AGTCCATGAT | AAGTTACCCA | 900 |
| AGCAGTTAAA | AGTGCATATA | AAAGAAGATA | AATATTCAGT | TGTAGGGAAG | 950 |
| GTTGCTACTG | GGAACTATAG | TAAAGTTCCT | TGGATTTCAA | TATATGATGA | 1000 |
| GAATATAACA | AAAGAAACAA | AGGATGGATA | TTATTTGGTA | TATCTTTTTC | 1050 |
| ATCCGGAAGG | AGAAGGCATA | TACTTATCTT | TGAATCAAGG | ATGGTCAAAG | 1100 |
| ATAAGTGATA | TGTT | | | | 1114 |

2) INFORMATION FOR SEQ ID NO: 179

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | CCATAGCAGA | ATATGAAAAA | 50 |
| CGTTTAGGCC | CATACACCAA | GATAGACATC | ATAGAAGTTC | CAGACGAAAA | 100 |
| AGCACCAGAA | AATATGAGCG | ACAAAGAAAT | TGAGCAAGTA | AAAGAAAAAG | 150 |
| AAGGCCAACG | AATACTAGCC | AAAATCAAAC | CACAATCCAC | AGTCATTACA | 200 |
| TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | GAAGGATTGG | CCCAAGAATT | 250 |
| GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | CTTTGTATTC | GTCATTGGCG | 300 |
| GATCAAACGG | CCTGCACAAG | GACGTCTTAC | AACGCAGTAA | CTATGCACTA | 350 |
| TCATTTAGCA | AAATGACATT | CCCACATCAA | ATGATGCGGG | TTGTGTTAAT | 400 |
| TGAACAAGTG | TATAGAGCAT | TTAAGATTAT | GCGTGGAGAA | GCATATCATA | 450 |
| AATGATGCGG | TTTTTTCAGC | CGCTTCATAA | AGGGATTTTG | AATGTATCAG | 500 |
| AACATATGAG | GTTTATGTGA | ATTGCTGTTA | TGTTTTTAAG | AAGCTTATCA | 550 |
| TAAGTAATGA | GGTTCATGAT | TTTTGACATA | GTTAGCCTCC | GCAGTCTTTC | 600 |
| ATTTCAAGTA | AATAATAGCG | AAATATTCTT | TATACTGAAT | ACTTATAGTG | 650 |
| AAGCAAAGTT | CTAGCTTTGA | GAAAATTCTT | TCTGCAACTA | AATATAGTAA | 700 |

| | | | | | |
|------------|-------------|------------|------------|------------|------|
| ATTACGGTAA | AATATAAATA | AGTACATATT | GAAGAAAATG | AGACATAATA | 750 |
| TATTTTATAA | TAGGAGGGAA | TTTCAAATGA | TAGACAACTT | TATGCAGGTC | 800 |
| CTTAAATTAA | TTAAAGAGAA | ACGTACCAAT | AATGTAGTTA | AAAAATCTGA | 850 |
| TTGGGATAAA | GGTGATCTAT | ATAAAACTTT | AGTCCATGAT | AAGTTACCCA | 900 |
| AGCAGTTAAA | AGTGCAATATA | AAAGAAGATA | AATATTCAGT | TGTAGGGAAG | 950 |
| GTTGCTACTG | GGAACATATAG | TAAAGTTCCT | TGGATTTCAT | TATATGATGA | 1000 |
| GAATATAACA | AAAGAAACAA | AGGATGGATA | TTATTTGGTA | TATCTTTTTC | 1050 |
| ATCCGGAAGG | AGAAGGCATA | TACTTATCTT | TGAATCAAGG | ATGGTCAAAG | 1100 |
| ATAAGTGATA | TGTTTCCGCG | G | | | 1121 |

2) INFORMATION FOR SEQ ID NO: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1121 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180

| | | | | | |
|------------|------------|-------------|------------|------------|------|
| TAGCTGTAGG | GAAACTAAAA | GAGAAATATT | GGAAGCAAGC | CATAGCAGAA | 50 |
| TATGAAAAAC | GTTTAGGCCC | ATACACCAAG | ATAGACATCA | TAGAAGTTCC | 100 |
| AGACGAAAAA | GCACCAGAAA | ATATGAGCGA | CAAAGAAATT | GAGCAAGTAA | 150 |
| AAGAAAAAGA | AGGCCAACGA | ATACTAGCCA | AAATCAAACC | ACAATCCACA | 200 |
| GTCATTACAT | TAGAAATACA | AGGAAAGATG | CTATCTTCCG | AAGGATTGGC | 250 |
| CCAAGAATTG | AACCAACGCA | TGACCCAAGG | GCAAAGCGAC | TTTGTATTCT | 300 |
| TCATTGGCGG | ATCAAACGGC | CTGCACAAGG | ACGTCTTACA | ACGCAGTAAC | 350 |
| TATGCACTAT | CATTTAGCAA | AATGACATTC | CCACATCAAA | TGATGCGGGT | 400 |
| TGTGTTAATT | GAACAAGTGT | ATAGAGCATT | TAAGATTATG | CGTGGAGAAG | 450 |
| CATATCATAA | ATGATGCGGT | TTTTTCAGCC | GCTTCATAAA | GGGATTTTGA | 500 |
| ATGTATCAGA | ACATATGAGG | TTTATGTGAA | TTGCTGTTAT | GTTTTTAAGA | 550 |
| AGCTTATCAT | AAGTAATGAG | GTTTCATGATT | TTTGACATAG | TTAGCCTCCG | 600 |
| CAGTCTTTCA | TTTCAAGTAA | ATAATAGCGA | AATATTCTTT | ATACTGAATA | 650 |
| CTTATAGTGA | AGCAAAGTTC | TAGCTTTGAG | AAAATTCTTT | CTGCAACTAA | 700 |
| ATATAGTAAA | TTACGGTAAA | ATATAAATAA | GTACATATTG | AAGAAAATGA | 750 |
| GACATAATAT | ATTTTATAAT | AGGAGGGAAT | TTCAAATGAT | AGACAACTTT | 800 |
| ATGCAGGTCC | TTAAATTAAT | TAAAGAGAAA | CGTACCAATA | ATGTAGTTAA | 850 |
| AAAATCTGAT | TGGGATAAAG | GTGATCTATA | TAAAACTTTA | GTCCATGATA | 900 |
| AGTTACCCAA | GCAGTTAAAA | GTGCATATAA | AAGAAGATAA | ATATTCAGTT | 950 |
| GTAGGGAAGG | TTGCTACTGG | GAACTATAGT | AAAGTTCCTT | GGATTTCAAT | 1000 |
| ATATGATGAG | AATATAACAA | AAGAAACAAA | GGATGGATAT | TATTTGGTAT | 1050 |
| ATCTTTTTCA | TCCGGAAGGA | GAAGGCATAT | ACTTATCTTT | GAATCAAGGA | 1100 |
| TGGTCAAAGA | TAAGTGATAT | G | | | 1121 |

2) INFORMATION FOR SEQ ID NO: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1131 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181

| | | | | | |
|------------|------------|------------|------------|-------------|------|
| CTGTAGGGAA | ACTAAAAGAG | AAATATTGGA | AGCAAGCCAT | AGCAGAATAT | 50 |
| GAAAAACGTT | TAGGCCCAT | CACCAAGATA | GACATCATAG | AAGTTCCAGA | 100 |
| CGAAAAAGCA | CCAGAAAATA | TGAGCGACAA | AGAAATTGAG | CAAGTAAAAG | 150 |
| AAAAAGAAGG | CCAACGAATA | CTAGCCAAAA | TCAAACCACA | ATCCACAGTC | 200 |
| ATTACATTAG | AAATACAAGG | AAAGATGCTA | TCTTCCGAAG | GATTGGCCCA | 250 |
| AGAATTGAAC | CAACGCATGA | CCCAAGGGCA | AAGCGACTTT | GTATTCGTCA | 300 |
| TTGGCGGATC | AAACGGCCTG | CACAAGGACG | TCTTACAACG | CAGTAACTAT | 350 |
| GCACTATCAT | TTAGCAAAAT | GACATTCCCA | CATCAAATGA | TGCGGGTTGT | 400 |
| GTTAATTGAA | CAAGTGTATA | GAGCATTTAA | GATTATGCGT | GGAGAAGCAT | 450 |
| ATCATAAATG | ATGCGGTTTT | TTCAGCCGCT | TCATAAAGGG | ATTTTGAATG | 500 |
| TATCAGAACA | TATGAGGTTT | ATGTGAATTG | CTGTTATGTT | TTTAAGAAGC | 550 |
| TTATCATAAG | TAATGAGGTT | CATGATTTTT | GACATAGTTA | GCCTCCGCAG | 600 |
| TCTTTCATTT | CAAGTAAATA | ATAGCGAAAT | ATTCTTTATA | CTGAATACTT | 650 |
| ATAGTGAAGC | AAAGTTCTAG | CTTTGAGAAA | ATTCTTTCTG | CAACTAAATA | 700 |
| TAGTAAATTA | CGGTAAAATA | TAAATAAGTA | CATATTGAAG | AAAATGAGAC | 750 |
| ATAATATATT | TTATAATAGG | AGGGAATTTT | AAATGATAGA | CAACTTTATG | 800 |
| CAGGTCCTTA | AATTAATTAA | AGAGAAACGT | ACCAATAATG | TAGTTAAAAA | 850 |
| ATCTGATTGG | GATAAAGGTG | ATCTATATAA | AACTTTAGTC | CATGATAAGT | 900 |
| TACCCAAGCA | GTTAAAAGTG | CATATAAAAG | AAGATAAATA | TTCAAGTTGTA | 950 |
| GGGAAGGTTG | CTACTGGGAA | CTATAGTAAA | GTTCTTGGGA | TTTCAATATA | 1000 |
| TGATGAGAAT | ATAACAAAAG | AAACAAAGGA | TGGATATTAT | TTGGTATATC | 1050 |
| TTTTTCATCC | GGAAGGAGAA | GGCATATACT | TATCTTTGAA | TCAAGGATGG | 1100 |
| TCAAAGATAA | GTGATATGTT | TCCGCGGGAT | A | | 1131 |

2) INFORMATION FOR SEQ ID NO: 182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CATTAGAAAT | ACAAGGAAAG | ATGCTATCTT | CCGAAGGATT | GGCCCAAGAA | 50 |
| TTGAACCAAC | GCATGACCCA | AGGGCAAAGC | GACTTTGTAT | TCGTCATTGG | 100 |
| CGGATCAAAC | GGCCTGCACA | AGGACGTCTT | ACAACGCAGT | AACTATGCAC | 150 |
| TATCATTTAG | CAAAATGACA | TTCCCACATC | AAATGATGCG | GGTTGTGTTA | 200 |
| ATTGAACAAG | TGTATAGAGC | ATTTAAGATT | ATGCGTGGAG | AAGCATATCA | 250 |
| TAAATGATGC | GGTTTTTTCA | GCCGCTTCAT | AAAGGGATTT | TGAATGTATC | 300 |
| AGAACATATG | AGGTTTATGT | GAATTGCTGT | TATGTTTTTA | AGAAGCTTAT | 350 |
| CATAAGTAAT | GAGGTTCATG | ATTTTTGACA | TAGTTAGCCT | CCGCAGTCTT | 400 |
| TCATTTCAAG | TAAATAATAG | CGAAATATTC | TTTATACTGA | ATACTTATAG | 450 |
| TGAAGCAAAG | TTCTAGCTTT | GAGAAAATTC | TTTCTGCAAC | TAAATATAGT | 500 |
| AAATTACGGT | AAAATATAAA | TAAGTACATA | TTGAAGAAAA | TGAGACATAA | 550 |
| TATATTTTAT | AATAGGAGGG | AATTTCAAAT | GATAGACAAC | TTTATGCAGG | 600 |
| TCCTTAAATT | AATTAAAGAG | AAACGTACCA | ATAATGTAGT | TAAAAAATCT | 650 |
| GATTGGGATA | AAGGTGATCT | ATATAAAACT | TTAGTCCATG | ATAAGTTACC | 700 |
| CAAGCAGTTA | AAAGTGCATA | TAAAAGAAGA | TAAATATTCA | GTTGTAGGGA | 750 |
| AGGTTGCTAC | TGGGAACAT | AGTAAAGTTC | CTTGGATTTC | AATATATGAT | 800 |
| GAGAATATAA | CAAAAGAAAC | AAAGGATGGA | TATTATTTGG | TATATCTTTT | 850 |
| TCATCCGGAA | GGAGAAGGCA | TATACTTATC | TTTGAATCAA | GGATGG | 896 |

2) INFORMATION FOR SEQ ID NO: 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183

| | | | | | |
|------------|-------------|------------|------------|------------|-----|
| GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | CCATATCAGA | ATATGAAAAA | 50 |
| CGTTTAGGCC | CATACACCAA | GATAGACATC | ATAGAAGTTC | CAGACGAAAA | 100 |
| AGCACCAGAA | AATATGAGCG | ACAAAGAAAT | CGAGCAAGTA | AAAGAAAAAG | 150 |
| AAGGCCAACG | AATACTAGCC | AAAATCAAAC | CACAATCAAC | AGTCATTACA | 200 |
| TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | GAAGGATTGG | CTCAAGAATT | 250 |
| GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | CTTTGTATTC | GTTATTGGCG | 300 |
| GATCAAACGG | CCTGCACAAG | GACGTCTTAC | AACGCAGTAA | CTATGCACTA | 350 |
| TCATTCAGCA | AAATGACATT | TCCACATCAG | ATGATGCGGG | TTGTGTTAAT | 400 |
| TGAGCAAGTG | TATAGAGCAT | TTAAGATTAT | GCGTGGGGAA | GCATATCATA | 450 |
| AATGATGCGG | TTTTTTCAGC | CGCTTCATAA | AGGGATTTTG | AATGTATCAG | 500 |
| AACATATGAG | GTTTATGTGA | ATTGCTGTTA | TGTTTTTAAG | AAGCTTATCA | 550 |
| TAAGTAATGA | GGTTCATGAT | TTTTGACATA | GTTAGCCTCC | GCAGTCTTTC | 600 |
| ATTTCAAGTA | AATAATAGCG | AAATATTCTT | TATACTGAAT | ACTTATAGTG | 650 |
| AAGCAAAGTT | CTAGCTTTGA | GAAAATTCTT | TCTGCAACTA | AATATAGTAA | 700 |
| ATTACGGTAA | AATATAAATA | AGTACATATT | GAAGAAAATG | AGACATAATA | 750 |
| TATTTTATAA | TAGGAGGGAA | TTTCAAATGA | TAGACAACCT | TATGCAGGTC | 800 |
| CTTAAATTAA | TTAAAGAGAA | ACGTACCAAT | AATGTAGTTA | AAAAATCTGA | 850 |
| TTGGGATAAA | GGTGATCTAT | ATAAACTTTT | AGTCCATGAT | AAGTTACCCA | 900 |
| AGCAGTTAAA | AGTGCAATATA | AAAGAAGATA | AATATTCAGT | TGTAGGGAAG | 950 |

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GTTGCTACTG | GGAAGTATAG | TAAAGTTCCT | TGGATTTCAA | TATATGATGA | 1000 |
| GAATATAACA | AAAGAAACAA | AGGATGGATA | TTATTTGGTA | TATCTTTTTC | 1050 |
| ATCCGGAAGG | AGAAGGCATA | TACTTATCTT | TGAATCAAGG | ATGGTCAAAG | 1100 |
| ATAAGTGATA | TGTTTCCGCG | GGATA | | | 1125 |

2) INFORMATION FOR SEQ ID NO: 184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATAAGAGGGA | ACAGTGTGAA | CAAGTTAATA | ACTTGTGGAT | AACTGGAAAG | 50 |
| TTGATAACAA | TTTGGAGGAC | CAAACGACAT | GAAAATCACC | ATTTTAGCTG | 100 |
| TAGGGAAACT | AAAAGAGAAA | TATTGGAAGC | AAGCCATAGC | AGAATATGAA | 150 |
| AAACGTTTAG | GCCCATACAC | CAAGATAGAC | ATCATAGAAG | TTCCAGACGA | 200 |
| AAAAGCACCA | GAAAATATGA | GCGACAAAGA | AATTGAGCAA | GTAAAAGAAA | 250 |
| AAGAAGGCCA | ACGAATACTA | GCCAAAATCA | AACCACAATC | CACAGTCATT | 300 |
| ACATTAGAAA | TACAAGGAAA | GATGCTATCT | TCCGAAGGAT | TGGCCCAAGA | 350 |
| ATTGAACCAA | CGCATGACCC | AAGGGCAAAG | CGACTTTGTA | TTCGTCATTG | 400 |
| GCGGATCAAA | CGGCCTGCAC | AAGGACGTCT | TACAACGCAG | TAAGTATGCA | 450 |
| CTATCATTTA | GCAAAATGAC | ATTCCCACAT | CAAATGATGC | GGGTTGTGTT | 500 |
| AATTGAACAA | GTGTATAGAG | CATTTAAGAT | TATGCGTGGA | GAGGCTTATC | 550 |
| ATAAATAAAA | CTAAAAATTA | GATTGTGTAT | AATTTAAAAA | TTTAATGAGA | 600 |
| TGTGGAGGAA | TTACATATAT | GAAATATTGG | AGTATACCTT | GCAATATCAT | 650 |
| ACGATGTTTA | TAGAGTGTTT | AATAAACCA | | | 679 |

2) INFORMATION FOR SEQ ID NO: 185

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1125 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185

93/125

| | | | | | |
|------------|-------------|------------|-------------|------------|------|
| GGAAACTAAA | AGAGAAATAT | TGGAAGCAAG | CCATAGCAGA | ATATGAAAAA | 50 |
| CGTTTAGGCC | CATACACCAA | GATAGACATC | ATAGAAGTTC | CAGACGAAAA | 100 |
| AGCACCAGAA | AATATGAGCG | ACAAAGAAAT | TGAGCAAGTA | AAAGAAAAAG | 150 |
| AAGGCCAACG | AATACTAGCC | AAAATCAAAC | CACAATCAAC | AGTCATTACA | 200 |
| TTAGAAATAC | AAGGAAAGAT | GCTATCTTCC | GAAGGATTGG | CACAAGAATT | 250 |
| GAACCAACGC | ATGACCCAAG | GGCAAAGCGA | CTTTGTATTTC | GTCATTGGCG | 300 |
| GATCAAACGG | CCTGCACAAG | GACGTCTTAC | AACGTAGTAA | CTACGCACTA | 350 |
| TCATTCAGCA | AAATGACATT | CCCACATCAA | ATGATGCGGG | TTGTGTTAAT | 400 |
| TGAGCAAGTG | TATAGAGCGT | TTAAGATTAT | GCGTGGAGAA | GCATATCATA | 450 |
| AATGATGCGG | TTTTTTTCAGC | CGCTTCATAA | AGGGATTTTG | AATGTATCAG | 500 |
| AACATATGAG | GTTTATGTGA | ATTGCTGTTA | TGTTTTTAAAG | AAGCTTATCA | 550 |
| TAAGTAATGA | GGTTCATGAT | TTTTGACATA | GTTAGCCTCC | GCAGTCTTTC | 600 |
| ATTTCAAGTA | AATAATAGCG | AAATATTCTT | TATACTGAAT | ACTTATAGTG | 650 |
| AAGCAAAGTT | CTAGCTTTGA | GAAAATTCTT | TCTGCAACTA | AATATAGTAA | 700 |
| ATTACGGTAA | AATATAAATA | AGTACATATT | GAAGAAAATG | AGACATAATA | 750 |
| TATTTTATAA | TAGGAGGGAA | TTTCAAATGA | TAGACAACTT | TATGCAGGTC | 800 |
| CTTAAATTAA | TTAAAGAGAA | ACGTACCAAT | AATGTAGTTA | AAAAATCTGA | 850 |
| TTGGGATAAA | GGTGATCTAT | ATAAAACTTT | AGTCCATGAT | AAGTTACCCA | 900 |
| AGCAGTTAAA | AGTGCAATATA | AAAGAAGATA | AATATTCAGT | TGTAGGGAAG | 950 |
| GTTGCTACTG | GGAACATATAG | TAAAGTTCCT | TGGATTTCAA | TATATGATGA | 1000 |
| GAATATAACA | AAAGAAACAA | AGGATGGATA | TTATTTGGTA | TATCTTTTTC | 1050 |
| ATCCGGAAGG | AGAAGGCATA | TACTTATCTT | TGAATCAAGG | ATGGTCAAAG | 1100 |
| ATAAGTGATA | TGTTTCCGCG | GGATA | | | 1125 |

2) INFORMATION FOR SEQ. ID NO: 186

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186

| | | | | | |
|------------|------------|------------|------------|-------------|-----|
| TACATTAGAA | ATACAAGGAA | AGATGCTATC | TTCCGAAGGA | TTGGCCCAAG | 50 |
| AATTGAACCA | ACGCATGACC | CAAGGGCAAA | GCGACTTTGT | ATTCGTCATT | 100 |
| GGCGGATCAA | ACGGCCTGCA | CAAGGACGTC | TTACAACGCA | GTAACATATGC | 150 |
| ACTATCATTT | AGCAAAATGA | CATTCCCACA | TCAAATGATG | CGGGTTGTGT | 200 |
| TAATTGAACA | AGTGTATAGA | GCATTTAAGA | TTATGCGTGG | AGAAGCATAT | 250 |
| CATAAATGAT | GCGGTTTTTT | CAGCCGCTTC | ATAAAGGGAT | TTTGAATGTA | 300 |
| TCAGAACATA | TGAGGTTTAT | GTGAATTGCT | GTTATGTTTT | TAAGAAGCTT | 350 |
| ATCATAAGTA | ATGAGGTTCA | TGATTTTTTG | CATAGTTAGC | CTCCGCAGTC | 400 |
| TTTCATTTCA | AGTAAATAAT | AGCGAAATAT | TCTTTATACT | GAATACTTAT | 450 |
| AGTGAAGCAA | AGTTCTAGCT | TTGAGAAAAT | TCTTTCTGCA | ACTAAATATA | 500 |
| GTAAATTACG | GTAAATATA | AATAAGTACA | TATTGAAGAA | AATGAGACAT | 550 |
| AATATATTTT | ATAATAGGAG | GGAATTTCAA | ATGATAGACA | ACTTTATGCA | 600 |
| GGTCCTTAAA | TTAATTAAAG | AGAAACGTAC | CAATAATGTA | GTAAAAAAT | 650 |
| CTGATTGGGA | TAAAGGTGAT | CTATATAAAA | CTTTAGTCCA | TGATAAGTTA | 700 |

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CCCAAGCAGT | TAAAAGTGCA | TATAAAAGAA | GATAAATATT | CAGTTGTAGG | 750 |
| GAAGGTTGCT | ACTGGGAAGT | ATAGTAAAGT | TCCTTGGATT | TCAATATATG | 800 |
| ATGAGAATAT | AACAAAAGAA | ACAAAGGATG | GATATTATTT | GGTATATCTT | 850 |
| TTTCATCCGG | AAGGAGAAGG | CATATACTTA | TCTTTGAATC | AAGGATGGTC | 900 |
| AAAGATAAGT | GATATGTTTC | CGCGGG | | | 926 |

2) INFORMATION FOR SEQ ID NO: 187

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187

GGATGTGGGT ATGCTAATGT TGTT 24

2) INFORMATION FOR SEQ ID NO: 188

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188

TGAACAATTT TATTTCTCAT ACCATAG 27

2) INFORMATION FOR SEQ ID NO: 189

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2154 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189

| | | | | | |
|------------|-------------|-------------|-------------|------------|------|
| CGGTAATAAA | AAATACGATA | TAGATGAATA | ACAAAACAGT | GAAGCAATCC | 50 |
| GTAACGATGG | TTGCTTCACT | GTTTTATTAT | GAATTATTAA | TAAGTGCTGT | 100 |
| TACTTCTCCC | TTAAATACAA | TTTCTTCATT | TTCATTGTAT | GTTGAAAGTG | 150 |
| ACACTGTAAC | GAGTCCATTT | TCTTTTTTTA | TGGATTTCTT | ATTTGTAATT | 200 |
| TCAGCGATAA | CGTACAATGT | ATTACCTGGG | TATACAGGTT | TAATAAATTT | 250 |
| AACGTTATTC | ATTTGTGTTC | CTGCTACAAC | TTCTTCTCCG | TATTTACCTT | 300 |
| CTTCTACCCA | TAATTTAAAT | GATATTGAAA | GTGTATGCAT | GCCAGATGCA | 350 |
| ATGATACCTT | TAAATCTACT | TTGTTCTGCT | TTTTCTTTAT | CTATATGCAT | 400 |
| ATATTGAGGA | TCAAAAGTTG | TTGCAAATTG | GATAATTTCT | TCTTCTGTAA | 450 |
| TATGAAGGCT | TTTTGTTTTG | AATGTTTCTC | CTACTATAAA | ATCATCGTAT | 500 |
| TTCATATATG | TCTCTCTTTC | TTATTCAAAT | TAATTTTTTA | GTATGTAACA | 550 |
| TGTTAAAGGT | AAGTCTACCG | TCACTGAAAC | GTAAGACTCA | CCTCTAACTT | 600 |
| TCTATTGAGA | CAAATGCACC | ATTTTATCTG | CATTGTCTGT | AAAGATACCA | 650 |
| TCAACTCCCC | AATTAGCAAG | TTGGTTTGCA | CGTGCTGGTT | TGTTTACAGT | 700 |
| CCATACGTTT | AATTCATAAC | CCGCTTCTTT | TACCATTTTT | ACTTTTGCTT | 750 |
| TAGTAAGTTT | GGCATCTTCA | GTGTTTACTA | TTTTAGCATT | ACAGTAATCT | 800 |
| AAAAGTGTTT | TCCAGTCTTC | ACGAAACGAA | GTTGTATGGA | ATATAACTGC | 850 |
| TCTGTTATAT | TGTGGCATGA | TTTCTTCTGC | AAGTTTAACA | AGCACAACAT | 900 |
| TAAAGCTTGA | AATGAGCACT | TCTTGATTCT | GATTTAAGTT | TGTTAATTGT | 950 |
| TCTTCCACTT | GCTTAACCAT | ACTTTTAGAA | AGTGCTAGTC | CATTCCGTCC | 1000 |
| AGTAATACCT | TTTAATTCTA | CATTTAAATT | CATATTATAT | TCATTTGCTA | 1050 |
| TTTTTACTAC | ATCATCGAAA | GTTGGCAAAT | GTTTCATCTT | GAATTTTTCA | 1100 |
| CCAAACCAAG | ATCCTGCAGA | AGCATCTTTA | ATTTTCATCAT | AATTCAATTC | 1150 |
| AGTTATTTCC | CCGGACATAT | TTGTAGTCCG | TTCTAAATAA | TCATCATGAA | 1200 |
| TGATAATCAG | TTGTTTCATCT | TTTGTAATTG | CAACATCTAA | CTCCAACCAG | 1250 |
| TTTATACCTT | CTACTTCTGA | AGCAGCTTTA | AATGATGCAA | TTGTATTTTC | 1300 |
| CGGAGCTTTA | CTAGGTAATC | CTCTATGTCC | ATATACAGTT | AGCATATTAC | 1350 |
| CTCTCCTTGC | ATTTTTATTT | TTTTAATTAA | CGTAACTGTA | TTATCACATT | 1400 |
| AATCGCACTT | TTATTTCCAT | TAAAAAGAGA | TGAATATCAT | AAATAAAGAA | 1450 |
| GTCGATAGAT | TCGTATTGAT | TATGGAGTTA | ATCTACGTCT | CATCTCATTT | 1500 |
| TTAAAAAATC | ATTTATGTCC | CAAGCTCCAT | TTTGTAATCA | AGTCTAGTTT | 1550 |
| TTCGGTTCTG | TTGCAAAGTT | GAATTTATAG | TATAATTTTA | ACAAAAAGGA | 1600 |
| GTCTTCTGTA | TGAACTATTT | CAGATATAAA | CAATTTAACA | AGGATGTTAT | 1650 |
| CACTGTAGCC | GTTGGCTACT | ATCTAAGATA | TACATTGAGT | TATCGTGATA | 1700 |
| TATCTGAAAT | ATTAAGGGAA | CGTGGTGTA | ACGTTTCATCA | TTCAACGGTC | 1750 |
| TACCGTTGGG | TTCAAGAATA | TGCCCCAATT | TTGTATCAAA | TTTGGAAGAA | 1800 |
| AAAGCATAAA | AAAGCTTATT | ACAAATGGCG | TATTGATGAG | ACGTACATCA | 1850 |
| AAATAAAAGG | AAAATGGAGC | TATTTATATC | GTGCCATTGA | TGCAGAGGGA | 1900 |
| CATACATTAG | ATATTTGGTT | GCGTAAGCAA | CGAGATAATC | ATTCAGCATA | 1950 |
| TGCGTTTATC | AAACGTCTCA | TTAAACAATT | TGGTAAACCT | CAAAAGGTAA | 2000 |
| TTACAGATCA | GGCACCTTCA | ACGAAGGTAG | CAATGGCTAA | AGTAATTAAA | 2050 |
| GCTTTTAAAC | TTAAACCTGA | CTGTCAATTGT | ACATCGAAAT | ATCTGAATAA | 2100 |
| CCTCATTGAG | CAAGATCACC | GTCATATTAA | AGTAAGAAAG | ACAAGGTATC | 2150 |
| AAAG | | | | | 2154 |

2) INFORMATION FOR SEQ ID NO: 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2410 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190

| | | | | | |
|-------------|------------|-------------|------------|------------|------|
| CCACCTTCAT | ATGACGTCTA | TCCATTTATG | TATGGCATGA | GTAACGAAGA | 50 |
| ATATAATAAA | TTAACCGAAG | ATAAAAAAGA | ACCTCTGCTC | AACAAGTTCC | 100 |
| AGATTACAAC | TTCACCAGGT | TCAACTCAAA | AAATATTTAA | AGCAATGATT | 150 |
| GGGTTAAATA | ACAAAACATT | AGACGATAAA | ACAAGTTATA | AAATCGATGG | 200 |
| TAAAGGTTGG | CAAAAAGATA | AATCTTGGGG | TGGTTACAAC | GTTACAAGAT | 250 |
| ATGAAGTGGT | AAATGGTAAT | ATCGACTTAA | AACAAGCAAT | AGAATCATCA | 300 |
| GATAACATTT | TCTTTGCTAG | AGTAGCACTC | GAATTAGGCA | GTAAGAAATT | 350 |
| TGAAAAAGGC | ATGAAAAAAC | TAGGTGTTGG | TGAAGATATA | CCAAGTGATT | 400 |
| ATCCATTTTA | TAATGCTCAA | ATTTCAAACA | AAAATTTAGA | TAATGAAATA | 450 |
| TTATTAGCTG | ATTCAGGTTA | CGGACAAGGT | GAAATACTGA | TTAACCCAGT | 500 |
| ACAGATCCTT | TCAATCTATA | GCGCATTAGA | AAATAATGGC | AATATTAACG | 550 |
| CACCTCACTT | ATTAAAAGAC | ACGAAAAACA | AAGTTTGGAA | GAAAAATATT | 600 |
| ATTTCCAAAG | AAAATATCAA | TCTATTAACT | GATGGTATGC | AACAAGTCGT | 650 |
| AAATAAAACA | CATAAAGAAG | ATATTTATAG | ATCTTATGCA | AACTTAATTG | 700 |
| GCAAATCCGG | TACTGCAGAA | CTCAAAATGA | AACAAGGAGA | AACTGGCAGA | 750 |
| CAAATTGGGT | GGTTTATATC | ATATGATAAA | GATAATCCAA | ACATGATGAT | 800 |
| GGCTATTAAT | GTTAAAGATG | TACAAGATAA | AGGAATGGCT | AGCTACAATG | 850 |
| CCAAAATCTC | AGGTAAAGTG | TATGATGAGC | TATATGAGAA | CGGTAATAAA | 900 |
| AAATACGATA | TAGATGAATA | ACAAAACAGT | GAAGCAATCC | GTAACGATGG | 950 |
| TTGCTTCACT | GTTTTATTAT | GAATTATTAA | TAAGTGCTGT | TACTTCTCCC | 1000 |
| TTAAATACAA | TTCTTTCATT | TTCATTGTAT | GTTGAAAGTG | ACACTGTAAC | 1050 |
| GAGTCCATTT | TCTTTTTTAA | TGGATTCTCT | ATTTGTAATT | TCAGCGATAA | 1100 |
| CGTACAATGT | ATTACCTGGG | TATACAGGTT | TAATAAATTT | AACGTTATTC | 1150 |
| ATTTGTGFTC | CTGCTACAAC | TTCTTCTCCG | TATTTACCTT | CTTCTACCCA | 1200 |
| TAATTTAAAT | GATATTGAAA | GTGTATGCAT | GCCAGATGCA | ATGATACCTT | 1250 |
| TAAATCTACT | TTGTTCTGCT | TTTTCTTTAT | CTATATGCAT | ATATTGAGGA | 1300 |
| TCAAAAGTTG | TTGCAAATTG | GATAATTTCT | TCTTCTGTAA | TATGAAGGCT | 1350 |
| TTTTGTTTTG | AATGTTTCTC | CTACTATAAA | ATCATCGTAT | TTCATATATG | 1400 |
| TCTCTCTTTC | TTATTCAAAT | TAATTTTTTA | GTATGTAACA | TGTTAAAGGT | 1450 |
| AAGTCTACCG | TCACTGAAAC | GTAAGACTCA | CCTCTAACTT | TCTATTGAGA | 1500 |
| CAAATGCACC | ATTTTATCTG | CATTGTCTGT | AAAGATACCA | TCAACTCCCC | 1550 |
| AATTAGCAAG | TTGGTTTGCA | CGTGCTGGTT | TGTTTACAGT | CCATACGTTT | 1600 |
| AATTCATAAC | CCGCTTCTTT | TACCATTTTT | ACTTTTGCTT | TAGTAAGTTT | 1650 |
| GGCATCTTCA | GTGTTTACTA | TTTTAGCATT | ACAGTAATCT | AAAAGTGTTT | 1700 |
| TCCAGTCTTC | ACGAAACGAA | GTTGTATGGA | ATATAACTGC | TCTGTTATAT | 1750 |
| TGTGGCATGA | TTTCTTCTGC | AAGTTTAAAC | AGCACACAT | TAAAGCTTGA | 1800 |
| AATGAGCACT | TCTTGATTCT | GATTTAAGTT | TGTTAATTGT | TCTTCCACTT | 1850 |
| GCTTAACCAT | ACTTTTAGAA | AGTGCTAGTC | CATTCGGTCC | AGTAATACCT | 1900 |
| TTTAATTCTA | CATTTAAATT | CATATTATAT | TCATTTGCTA | TTTTTACTAC | 1950 |
| ATCATCGAAA | GTTGGCAAAT | GTTTCATCTT | GAATTTTTC | CCAAACCAAG | 2000 |
| ATCCTGCAGA | AGCATCTTTA | ATTTTCATCAT | AATTCATTC | AGTTATTTCC | 2050 |
| CCGGACATAT | TTGTAGTCCG | TTCTAAATAA | TCATCATGAA | TGATAATCAG | 2100 |
| TTGTTTCATCT | TTTGTAATTG | CAACATCTAA | CTCCAACCAG | TTTATACCTT | 2150 |
| CTACTTCTGA | AGCAGCTTTA | AATGATGCAA | TTGTATTTTC | CGGAGCTTTA | 2200 |
| CTAGGTAATC | CTCTATGTCC | ATATACAGTT | AGCATATTAC | CTCTCCTTGC | 2250 |
| ATTTTTTATTT | TTTTAATTAA | CGTAACTGTA | TTATCACATT | AATCGCACTT | 2300 |
| TTATTTCCAT | TAAAAAGAGA | TGAATATCAT | AAATAAGAA | GTCGATAGAT | 2350 |
| TCGTATTGAT | TATGGAGTTA | ATCTACGTCT | CATCTCATTT | TTAAAAAATC | 2400 |
| ATTTATGTCC | | | | | 2410 |

2) INFORMATION FOR SEQ ID NO: 191

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191

| | | | | | |
|------------|-------------|-------------|------------|------------|------|
| CACCTTCATA | TGACGTCTAT | CCATTTATGT | ATGGCATGAG | TAACGAAGAA | 50 |
| TATAATAAAT | TAACCGAAGA | TAAAAAAGAA | CCTCTGCTCA | ACAAGTTCCA | 100 |
| GATTACAAC | TCACCAGGTT | CAACTCAAAA | AATATTAACA | GCAATGATTG | 150 |
| GGTTAAATAA | CAAAACATTA | GACGATAAAA | CAAGTTATAA | AATCGATGGT | 200 |
| AAAGGTTGGC | AAAAAGATAA | ATCTTGGGGT | GGTTACAACG | TTACAAGATA | 250 |
| TGAAGTGGTA | AATGGTAATA | TCGACTTAAA | ACAAGCAATA | GAATCATCAG | 300 |
| ATAACATTTT | CTTTGCTAGA | GTAGCACTCG | AATTAGGCAG | TAAGAAATTT | 350 |
| GAAAAAGGCA | TGAAAAAACT | AGGTGTTGGT | GAAGATATAC | CAAGTGATTA | 400 |
| TCCATTTTAT | AATGCTCAAA | TTTCAAACAA | AAATTTAGAT | AATGAAATAT | 450 |
| TATTAGCTGA | TTCAGGTTAC | GGACAAGGTG | AAATACTGAT | TAACCCAGTA | 500 |
| CAGATCCTTT | CAATCTATAG | CGCATTAGAA | AATAATGGCA | ATATTAACGC | 550 |
| ACCTCACTTA | TTAAAAGACA | CGAAAAACAA | AGTTTGGAAG | AAAAATATTA | 600 |
| TTTCCAAAGA | AAATATCAAT | CTATTAAGTG | ATGGTATGCA | ACAAGTCGTA | 650 |
| AATAAAACAC | ATAAAGAAGA | TATTTATAGA | TCTTATGCAA | ACTTAATTGG | 700 |
| CAAATCCGGT | ACTGCAGAAC | TCAAAATGAA | ACAAGGAGAA | ACTGGCAGAC | 750 |
| AAATTGGGTG | GTTTATATCA | TATGATAAAG | ATAATCCAAA | CATGATGATG | 800 |
| GCTATTAATG | TTAAAGATGT | ACAAGATAAA | GGAATGGCTA | GCTACAATGC | 850 |
| CAAATCTCA | GGTAAAGTGT | ATGATGAGCT | ATATGAGAAC | GGTAATAAAA | 900 |
| AATACGATAT | AGATGAATAA | CAAAACAGTG | AAGCAATCCG | TAACGATGGT | 950 |
| TGCTTCACTG | TTTTATTATG | AATTATTAAT | AAGTGCTGTT | ACTTCTCCCT | 1000 |
| TAAATACAAT | TTCTTCATTT | TCATTGTATG | TTGAAAGTGA | CACTGTAACG | 1050 |
| AGTCCATTTT | CTTTTTTTTAT | GGATTTCTTA | TTTGTAATTT | CAGCGATAAC | 1100 |
| GTACAATGTA | TTACCTGGGT | ATACAGGTTT | AATAAATTTA | ACGTTATTCA | 1150 |
| TTTGTGTTCC | TGCTACAAC | TCTTCTCCGT | ATTTACCTTC | TTCTACCCAT | 1200 |
| AATTTAAATG | ATATTGAAAG | TGTATGCATG | CCAGATGCAA | TGATACCTTT | 1250 |
| AAATCTACTT | TGTTCTGCTT | TTTCTTTATC | TATATGCATA | TATTGAGGAT | 1300 |
| CAAAAGTTGT | TGCAAATTGG | ATAATTTCTT | CTTCTGTAAT | ATGAAGGCTT | 1350 |
| TTTGTTTTGA | ATGTTTCTCC | TACTATAAAA | TCATCGTATT | TCATATATGT | 1400 |
| CTCTCTTTCT | TATTCAAATT | AATTTTTTTAG | TATGTAACAT | GTAAAGGTA | 1450 |
| AGTCTACCGT | CACTGAAACG | TAAGACTCAC | CTCTAACTTT | CTATTGAGAC | 1500 |
| AAATGCACCA | TTTTATCTGC | ATTGTCTGTA | AAGATACCAT | CAACTCCCCA | 1550 |
| ATTAGCAAGT | TGGTTTGCAC | GTGCTGGTTT | GTTTACAGTC | CATACGTTCA | 1600 |
| ATTCATAACC | CGCTTCTTTT | ACCATTTTTA | CTTTTGCTTT | AGTAAGTTTG | 1650 |
| GCATCTTCAG | TGTTTACTAT | TTTAGCATT | CAGTAATCTA | AAAGTGTTCT | 1700 |
| CCAGTCTTCA | CGAAACGAAG | TTGTATGGAA | TATAACTGCT | CTGTTATATT | 1750 |
| GTGGCATGAT | TTCTTCTGCA | AGTTTAACAA | GCACAACATT | AAAGCTTGAA | 1800 |
| ATGAGCACTT | CTTGATTCTG | ATTTAAGTTT | GTTAATTGTT | CTTCCACTTG | 1850 |
| CTTAACCA | | | | | 1858 |

2) INFORMATION FOR SEQ ID NO: 192

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192

| | | | | | |
|------------|------------|------------|------------|------------|------|
| CCACCTTCAT | ATGACGTCTA | TCCATTTATG | TATGGCATGA | GTAACGAAGA | 50 |
| ATATAATAAA | TTAACCGAAG | ATAAAAAAGA | ACCTCTGCTC | AACAAGTTCC | 100 |
| AGATTACAAC | TTCACCAGGT | TCAACTCAAA | AAATATTAAC | AGCAATGATT | 150 |
| GGGTTAAATA | ACAAAACATT | AGACGATAAA | ACAAGTTATA | AAATCGATGG | 200 |
| TAAAGGTTGG | CAAAAAGATA | AATCTTGGGG | TGGTTACAAC | GTTACAAGAT | 250 |
| ATGAAGTGGT | AAATGGTAAT | ATCGACTTAA | AACAAGCAAT | AGAATCATCA | 300 |
| GATAACATTT | TCTTTGCTAG | AGTAGCACTC | GAATTAGGCA | GTAAGAAATT | 350 |
| TGAAAAAGGC | ATGAAAAAAC | TAGGTGTTGG | TGAAGATATA | CCAAGTGATT | 400 |
| ATCCATTTTA | TAATGCTCAA | ATTTCAAACA | AAAATTTAGA | TAATGAAATA | 450 |
| TTATTAGCTG | ATTCAGGTTA | CGGACAAGGT | GAAATACTGA | TTAACCCAGT | 500 |
| ACAGATCCTT | TCAATCTATA | GCGCATTAGA | AAATAATGGC | AATATTAACG | 550 |
| CACCTCACTT | ATTAAAAGAC | ACGAAAAACA | AAGTTTGGAA | GAAAAATATT | 600 |
| ATTTCCAAAG | AAAATATCAA | TCTATTAACT | GATGGTATGC | AACAAGTCGT | 650 |
| AAATAAAACA | CATAAAGAAG | ATATTTATAG | ATCTTATGCA | AACTTAATTG | 700 |
| GCAAATCCGG | TACTGCAGAA | CTCAAAATGA | AACAAGGAGA | AACTGGCAGA | 750 |
| CAAATTGGGT | GGTTTATATC | ATATGATAAA | GATAATCCAA | ACATGATGAT | 800 |
| GGCTATTAAT | GTTAAAGATG | TACAAGATAA | AGGAATGGCT | AGCTACAATG | 850 |
| CCAAAATCTC | AGGTAAAGTG | TATGATGAGC | TATATGAGAA | CGGTAATAAA | 900 |
| AAATACGATA | TAGATGAATA | ACAAAACAGT | GAAGCAATCC | GTAACGATGG | 950 |
| TTGCTTCACT | GTTTTATTAT | GAATTATTAA | TAAGTGCTGT | TACTTCTCCC | 1000 |
| TTAAATACAA | TTTCTTCATT | TTCATTGTAT | GTTGAAAGTG | ACACTGTAAC | 1050 |
| GAGTCCATTT | TCTTTTTTTA | TGGATTTCTT | ATTTGTAATT | TCAGCGATAA | 1100 |
| CGTACAATGT | ATTACCTGGG | TATACAGGTT | TAATAAATTT | AACGTTATTC | 1150 |
| ATTTGTGTTC | CTGCTACAAC | TTCTTCTCCG | TATTTACCTT | CTTCTACCCA | 1200 |
| TAATTTAAAT | GATATTGAAA | GTGTATGCAT | GCCAGATGCA | ATGATACCTT | 1250 |
| TAAATCTACT | TTGTTCTGCT | TTTTCTTTAT | CTATATGCAT | ATATTGAGGA | 1300 |
| TCAAAAGTTG | TTGCAAATTG | GATAATTTCT | TCTTCTGTAA | TATGAAGGCT | 1350 |
| TTTTGTTTTG | AATGTTTCTC | CTACTATAAA | ATCATCGTAT | TTCATATATG | 1400 |
| TCTCTCTTTC | TTATTCAAAT | TAATTTTTTA | GTATGTAACA | TGTTAAAGGT | 1450 |
| AAGTCTACCG | TCACTGAAAC | GTAAGACTCA | CCTCTAACTT | TCTATTGAGA | 1500 |
| CAAATGCACC | ATTTTATCTG | CATTGTCTGT | AAAGATACCA | TCAACTCCCC | 1550 |
| AATTAGCAAG | TTGGTTTGCA | CGTGCTGGTT | TGTTTACAGT | CCATACGTTC | 1600 |
| AATTCATAAC | CCGCTTCTTT | TACCATTTTT | ACTTTTGCTT | TAGTAAGTTT | 1650 |
| GGCATCTTCA | GTGTTTACTA | TTTTAGCATT | ACAGTAATCT | AAAAGTGTTT | 1700 |
| TCCAGTCTTC | ACGAAACGAA | GTTGTATGGA | ATATAACTGC | TCTGTTATAT | 1750 |
| TGTGGCATGA | TTTCTTCTGC | AAGTTTAACA | AGCACACAT | TAAAGCTTGA | 1800 |
| AATGAGCACT | TCTTGATTCT | GATTTAAGTT | TGTTAATTGT | TCTTCCACTT | 1850 |
| GCTTAACCAT | A | | | | 1861 |

2) INFORMATION FOR SEQ ID NO: 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1861 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193

| | | | | | |
|------------|------------|------------|-------------|------------|------|
| CCACCTTCAT | ATGACGTCTA | TCCATTTATG | TATGGCATGA | GTAACGAAGA | 50 |
| ATATAATAAA | TTAACCGAAG | ATAAAAAAGA | ACCTCTGCTC | AACAAGTTCC | 100 |
| AGATTACAAC | TTCACCAGGT | TCAACTCAAA | AAATATTAAC | AGCAATGATT | 150 |
| GGGTTAAATA | ACAAAACATT | AGACGATAAA | ACAAGTTATA | AAATCGATGG | 200 |
| TAAAGGTTGG | CAAAAAGATA | AATCTTGGGG | TGGTTACAAC | GTTACAAGAT | 250 |
| ATGAAGTGGT | AAATGGTAAT | ATCGACTTAA | AACAAGCAAT | AGAATCATCA | 300 |
| GATAACATTT | TCTTTGCTAG | AGTAGCACTC | GAATTAGGCA | GTAAGAAATT | 350 |
| TGAAAAAGGC | ATGAAAAAAC | TAGGTGTTGG | TGAAGATATA | CCAAGTGATT | 400 |
| ATCCATTTTA | TAATGCTCAA | ATTTCAAACA | AAAATTTAGA | TAATGAAATA | 450 |
| TTATTAGCTG | ATTCAGGTTA | CGGACAAGGT | GAAATACTGA | TTAACCCAGT | 500 |
| ACAGATCCTT | TCAATCTATA | GCGCATTAGA | AAATAATGGC | AATATTAACG | 550 |
| CACCTCACTT | ATTAAAAGAC | ACGAAAAACA | AAGTTTGGAA | GAAAAATATT | 600 |
| ATTTCCAAAG | AAAATATCAA | TCTATTAACT | GATGGTATGC | AACAAGTCGT | 650 |
| AAATAAAACA | CATAAAGAAG | ATATTTATAG | ATCTTATGCA | AACTTAATTG | 700 |
| GCAAATCCGG | TACTGCAGAA | CTCAAAATGA | AACAAGGAGA | AACTGGCAGA | 750 |
| CAAATTGGGT | GGTTTATATC | ATATGATAAA | GATAATCCAA | ACATGATGAT | 800 |
| GGCTATTAAT | GTTAAAGATG | TACAAGATAA | AGGAATGGCT | AGCTACAATG | 850 |
| CCAAAATCTC | AGGTAAAGTG | TATGATGAGC | TATATGAGAA | CGGTAATAAA | 900 |
| AAATACGATA | TAGATGAATA | ACAAAACAGT | GAAGCAATCC | GTAACGATGG | 950 |
| TTGCTTCACT | GTTTTATTAT | GAATTATTAA | TAAGTGCTGT | TACTTCTCCC | 1000 |
| TTAAATACAA | TTTCTTCATT | TTCATTGTAT | GTTGAAAGTG | AACTGTAAAC | 1050 |
| GAGTCCATTT | TCTTTTTTTA | TGGATTTCTT | ATTTGTAATT | TCAGCGATAA | 1100 |
| CGTACAATGT | ATTACCTGGG | TATACAGGTT | TAATAAATTT | AACGTTATTC | 1150 |
| ATTTGTGTTC | CTGCTACAAC | TTCTTCTCCG | TATTTACCTT | CTTCTACCCA | 1200 |
| TAATTTAAAT | GATATTGAAA | GTGTATGCAT | GCCAGATGCA | ATGATACCTT | 1250 |
| TAAATCTACT | TTGTTCTGCT | TTTTCTTTAT | CTATATGCAT | ATATTGAGGA | 1300 |
| TCAAAAGTTG | TTGCAAATTG | GATAATTTCT | TCTTCTGTAA | TATGAAGGCT | 1350 |
| TTTTGTTTTG | AATGTTTCTC | CTACTATAAA | ATCATCGTAT | TTCATATATG | 1400 |
| TCTCTCTTTC | TTATTCAAAT | TAATTTTTTA | GTATGTAACA | TGTTAAAGGT | 1450 |
| AAGTCTACCG | TCACTGAAAC | GTAAGACTCA | CCTCTAACTT | TCTATTGAGA | 1500 |
| CAAATGCACC | ATTTTATCTG | CATTGTCTGT | AAAGATACCA | TCAACTCCCC | 1550 |
| AATTAGCAAG | TTGGTTTGCA | CGTGCTGGTT | TGTTTACAGT | CCATACGTTT | 1600 |
| AATTCATAAC | CCGCTTCTTT | TACCATTTTT | ACTTTTGCTT | TAGTAAGTTT | 1650 |
| GGCATCTTCA | GTGTTTACTA | TTTTAGCATT | ACAGTAATCT | AAAAGTGTTT | 1700 |
| TCCAGTCTTC | ACGAAACGAA | GTTGTATGGA | ATATAACTGC | TCTGTTATAT | 1750 |
| TGTGGCATGA | TTTCTTCTGC | AAGTTTAAAC | AGCACAAACAT | TAAAGCTTGA | 1800 |
| AATGAGCACT | TCTTGATTCT | GATTTAAGTT | TGTTAATTGT | TCTTCCACTT | 1850 |
| GCTTAACCAT | A | | | | 1861 |

2) INFORMATION FOR SEQ ID NO: 194

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1052 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194

| | | | | | |
|------------|------------|------------|------------|-------------|------|
| CGGTAATAAA | AAATACGATA | TAGATGAATA | ACAAAACAGT | GAAGCAATCC | 50 |
| GTAACGATGG | TTGCTTCACT | GTTTTATTAT | GAATTATTAA | TAAGTGCTGT | 100 |
| TACTTCTCCC | TTAAATACAA | TTTCTTCATT | TTCATTGTAT | GTTGAAAGTG | 150 |
| ACACTGTAAC | GAGTCCATTT | TCTTTTTTTA | TGGATTTCTT | ATTTGTAATT | 200 |
| TCAGCGATAA | CGTACAATGT | ATTACCTGGG | TATACAGGTT | TAATAAATTT | 250 |
| AACGTTATTC | ATTTGTGTTC | CTGCTACAAC | TTCTTCTCCG | TATTTACCTT | 300 |
| CTTCTACCCA | TAATTTAAAT | GATATTGAAA | GTGTATGCAT | GCCAGATGCA | 350 |
| ATGATACCTT | TAAATCTACT | TTGTTCTGCT | TTTTCTTTAT | CTATATGCAT | 400 |
| ATATTGAGGA | TCAAAGTTG | TTGCAAATTG | GATAATTTCT | TCTTCTGTAA | 450 |
| TATGAAGGCT | TTTTGTTTTG | AATGTTTCTC | CTACTATAAA | ATCATCGTAT | 500 |
| TTCATATATG | TCTCTCTTTC | TTATTCAAAT | TAATTTTTTA | GTATGTAACA | 550 |
| TGTTAAAGGT | AAGTCTACCG | TCACTGAAAC | GTAAGACTCA | CCTCTAACTT | 600 |
| TCTATTGAGA | CAAATGCACC | ATTTTATCTG | CATTGTCTGT | AAAGATACCA | 650 |
| TCAACTCCCC | AATTAGCAAG | TTGGTTTGCA | CGTGCTGGTT | TGTTTACAGT | 700 |
| CCATACGTTT | AATTCATAAC | CCGCTTCTTT | TACCATTTTT | ACTTTTGCTT | 750 |
| TAGTAAGTTT | GGCATCTTCA | GTGTTTACTA | TTTTAGCATT | ACAGTAATCT | 800 |
| AAAAGTGTTT | TCCAGTCTTC | ACGAAACGAA | GTTGTATGGA | ATATAACTGC | 850 |
| TCTGTTATAT | TGTGGCATGA | TTTCTTCTGC | AAGTTTAACA | AGCACAACAT | 900 |
| TAAAGCTTGA | AATGAGCACT | TCTTGATTCT | GATTTAAGTT | TGTTAATTGT | 950 |
| TCTTCCACTT | GCTTAACCAT | ACTTTTAGAA | AGTGCTAGTC | CATTCCGGTCC | 1000 |
| AGTAATACCT | TTTAATTCTA | CATTTAAATT | CATATTATAT | TCATTTGCTA | 1050 |
| TT | | | | | 1052 |

2) INFORMATION FOR SEQ ID NO: 195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3101 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: CCRI-9770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195

| | | | | | |
|------------|------------|------------|------------|------------|------|
| CTTCATATGA | CGTCTATCCA | TTTATGTATG | GCATGAGTAA | CGAAGAATAT | 50 |
| AATAAATTAA | CCGAAGATAA | AAAAGAACCT | CTGCTCAACA | AGTTCCAGAT | 100 |
| TACAACTTCA | CCAGGTTCAA | CTCAAAAAAT | ATTAACAGCA | ATGATTGGGT | 150 |
| TAAATAACAA | AACATTAGAC | GATAAAACAA | GTTATAAAAT | CGATGGTAAA | 200 |
| GGTTGGCAAA | AAGATAAATC | TTGGGGTGGT | TACAACGTTA | CAAGATATGA | 250 |
| AGTGGTAAAT | GGTAATATCG | ACTTAAAACA | AGCAATAGAA | TCATCAGATA | 300 |
| ACATTTTCTT | TGCTAGAGTA | GCACTCGAAT | TAGGCAGTAA | GAAATTTGAA | 350 |
| AAAGGCATGA | AAAACTAGG | TGTTGGTGAA | GATATACCAA | GTGATTATCC | 400 |
| ATTTTATAAT | GCTCAAATTT | CAAACAAAAA | TTTAGATAAT | GAAATATTAT | 450 |
| TAGCTGATTC | AGGTTACGGA | CAAGGTGAAA | TACTGATTAA | CCCAGTACAG | 500 |
| ATCCTTTCAA | TCTATAGCGC | ATTAGAAAAT | AATGGCAATA | TTAACGCACC | 550 |
| TCACTTATTA | AAAGACACGA | AAAACAAAGT | TTGGAAGAAA | AATATTATTT | 600 |
| CCAAAGAAAA | TATCAATCTA | TTAACTGATG | GTATGCAACA | AGTCGTAAAT | 650 |
| AAAACACATA | AAGAAGATAT | TTATAGATCT | TATGCAAAC | TAATTGGCAA | 700 |
| ATCCGGTACT | GCAGAACTCA | AAATGAAACA | AGGAGAAACT | GGCAGACAAA | 750 |
| TTGGGTGGTT | TATATCATAT | GATAAAGATA | ATCCAAACAT | GATGATGGCT | 800 |
| ATTAATGTTA | AAGATGTACA | AGATAAAGGA | ATGGCTAGCT | ACAATGCCAA | 850 |
| AATCTCAGGT | AAAGTGTATG | ATGAGCTATA | TGAGAACGGT | AATAAAAAAT | 900 |
| ACGATATAGA | TGAATAACAA | AACAGTGAAG | CAATCCGTAA | CGATGGTTGC | 950 |
| TTCACTGTTT | TATTATGAAT | TATTAATAAG | TGCTGTACT | TCTCCCTTAA | 1000 |
| ATACAATTTT | TTCATTTTCA | TTGTATGTTG | AAAGTGACAC | TGTAACGAGT | 1050 |
| CCATTTTCTT | TTTTTATGGA | TTTCTTATTT | GTAATTTTCA | CGATAACGTA | 1100 |
| CAATGTATTA | CCTGGGTATA | CAGGTTTAA | AAATTTAACG | TTATTCATTT | 1150 |
| GTGTTCTTGC | TACAACTTCT | TCTCCGTATT | TACCTTCTTC | TACCCATAAT | 1200 |
| TTAAATGATA | TTGAAAGTGT | ATGCATGCCA | GATGCAATGA | TACCTTTAAA | 1250 |
| TCTACTTTGT | TCTGCTTTTT | CTTTATCTAT | ATGCATATAT | TGAGGATCAA | 1300 |
| AAGTTGTTGC | AAATTGGATA | ATTTCTTCTT | CTGTAATATG | AAGGCTTTTT | 1350 |
| GTTTTGAATG | TTTCTCCTAC | TATAAAATCA | TCGTATTTCA | TATATGTCTC | 1400 |
| TCTTTCTTAT | TCAAATTAAT | TTTTTAGTAT | GTAACATGTT | AAAGGTAAGT | 1450 |
| CTACCGTCAC | TGAAACGTAA | GACTCACCTC | TAACTTTCTA | TTGAGACAAA | 1500 |
| TGCACCATTT | TATCTGCATT | GTCTGTAAAG | ATACCATCAA | CTCCCCAATT | 1550 |
| AGCAAGTTGG | TTTGCACGTG | CTGGTTTGTT | TACAGTCCAT | ACGTTCAATT | 1600 |
| CATAACCCGC | TTCTTTTACC | ATTTTACTT | TTGCTTTAGT | AAGTTTGGCA | 1650 |
| TCTTCAGTGT | TTACTATTTT | AGCATTACAG | TAATCTAAAA | GTGTTCTCCA | 1700 |
| GTCTTCACGA | AACGAAGTTG | TATGGAATAT | AACTGCTCTG | TTATATTGTG | 1750 |
| GCATGATTTT | TTCTGCAAGT | TTAACAAGCA | CAACATTAAA | GCTTGAAATG | 1800 |
| AGCACTTCTT | GATTCTGATT | TAAGTTTGTT | AATTGTTCTT | CCACTTGCTT | 1850 |
| AACCATACTT | TTAGAAAGTG | CTAGTCCATT | CGGTCCAGTA | ATACCTTTTA | 1900 |
| ATTCTACATT | TAAATTCATA | TTATATTCAT | TTGCTATTTT | TACTACATCA | 1950 |
| TCGAAAGTTG | GCAAATGTTT | ATCTTTGAAT | TTTTACCAA | ACCAAGATCC | 2000 |
| TGCAGAAGCA | TCTTTAATTT | CATCATAATT | CAATTCAGTT | ATTTCCCCGG | 2050 |
| ACATATTTGT | AGTCCGTTCT | AAATAATCAT | CATGAATGAT | AATCAGTTGT | 2100 |
| TCATCTTTTG | TAATTGCAAC | ATCTAACTCC | AACCAGTTTA | TACCTTCTAC | 2150 |
| TTCTGAAGCA | GCTTTAAATG | ATGCAATTGT | ATTTTCCGGA | GCTTTACTAG | 2200 |
| GTAATCCTCT | ATGTCCATAT | ACAGTTAGCA | TATTACCTCT | CCTTGCAATT | 2250 |
| TTATTTTTTT | AATTAACGTA | ACTGTATTAT | CACATTAATC | GCACTTTTAT | 2300 |
| TTCCATTAAA | AAGAGATGAA | TATCATAAAT | AAAGAAGTCG | ATAGATTCGT | 2350 |
| ATTGATTATG | GAGTTAATCT | ACGTCTCATC | TCATTTTTTA | AAAATCATTT | 2400 |
| ATGTCCCAAG | CTCCATTTTG | TAATCAAGTC | TAGTTTTTTC | GTTCTGTTGC | 2450 |
| AAAGTTGAAT | TTATAGTATA | ATTTTAACAA | AAAGGAGTCT | TCTGTATGAA | 2500 |
| CTATTTTCTA | TATAAACAAT | TTAACAAGGA | TGTTATCACT | GTAGCCGTTG | 2550 |
| GCTACTATCT | AAGATATACA | TTGAGTTATC | GTGATATATC | TGAAATATTA | 2600 |
| AGGGAACGTG | GTGTAAACGT | TCATCATTTA | ACGGTCTACC | GTTGGGTTCA | 2650 |
| AGAATATGCC | CCAATTTTGT | ATCAAATTTG | GAAGAAAAAG | CATAAAAAAG | 2700 |
| CTTATTACAA | ATGGCGTATT | GATGAGACGT | ACATCAAAT | AAAAGGAAAA | 2750 |

| | | | | | |
|------------|------------|------------|------------|------------|------|
| TGGAGCTATT | TATATCGTGC | CATTGATGCA | GAGGGACATA | CATTAGATAT | 2800 |
| TTGGTTGCGT | AAGCAACGAG | ATAATCATTC | AGCATATGCG | TTTATCAAAC | 2850 |
| GTCTCATTA | ACAATTTGGT | AAACCTCAAA | AGGTAATTAC | AGATCAGGCA | 2900 |
| CCTTCAACGA | AGGTAGCAAT | GGCTAAAGTA | ATTAAAGCTT | TTAAACTTAA | 2950 |
| ACCTGACTGT | CATTGTACAT | CGAAATATCT | GAATAACCTC | ATTGAGCAAG | 3000 |
| ATCACCGTCA | TATTAAAGTA | AGAAAGACAA | GGTATCAAAG | TATCAATACA | 3050 |
| GCAAAGAATA | CTTTAAAAGG | TATTGAATGT | ATTTACGCTC | TATATAAAAA | 3100 |
| G | | | | | 3101 |

2) INFORMATION FOR SEQ ID NO: 196

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3506 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196

| | | | | | |
|------------|------------|------------|------------|------------|------|
| CCACCTTCAT | ATGACGTCTA | TCCATTTATG | TATGGCATGA | GTAACGAAGA | 50 |
| ATATAATAAA | TTAACCGAAG | ATAAAAAAGA | ACCTCTGCTC | AACAAGTTCC | 100 |
| AGATTACAAC | TTCACCAGGT | TCAACTCAAA | AAATATTAAC | AGCAATGATT | 150 |
| GGGTTAAATA | ACAAAACATT | AGACGATAAA | ACAAGTTATA | AAATCGATGG | 200 |
| TAAAGGTTGG | CAAAAAGATA | AATCTTGGGG | TGGTTACAAC | GTTACAAGAT | 250 |
| ATGAAGTGGT | AAATGGTAAT | ATCGACTTAA | AACAAGCAAT | AGAATCATCA | 300 |
| GATAACATTT | TCTTTGCTAG | AGTAGCACTC | GAATTAGGCA | GTAAGAAATT | 350 |
| TGAAAAAGGC | ATGAAAAAAC | TAGGTGTTGG | TGAAGATATA | CCAAGTGATT | 400 |
| ATCCATTTTA | TAATGCTCAA | ATTTCAAACA | AAAATTTAGA | TAATGAAATA | 450 |
| TTATTAGCTG | ATTCAGGTTA | CGGACAAGGT | GAAATACTGA | TTAACCCAGT | 500 |
| ACAGATCCTT | TCAATCTATA | GCGCATTAGA | AAATAATGGC | AATATTAACG | 550 |
| CACCTCACTT | ATTAAAAGAC | ACGAAAAACA | AAGTTTGGAA | GAAAAATATT | 600 |
| ATTTCCAAAG | AAAATATCAA | TCTATTAACT | GATGGTATGC | AACAAGTCGT | 650 |
| AAATAAAACA | CATAAAGAAG | ATATTTATAG | ATCTTATGCA | AACTTAATTG | 700 |
| GCAAATCCGG | TACTGCAGAA | CTCAAAATGA | AACAAGGAGA | AACTGGCAGA | 750 |
| CAAATTGGGT | GGTTTATATC | ATATGATAAA | GATAATCCAA | ACATGATGAT | 800 |
| GGCTATTAAT | GTTAAAGATG | TACAAGATAA | AGGAATGGCT | AGCTACAATG | 850 |
| CCAAAATCTC | AGGTAAAGTG | TATGATGAGC | TATATGAGAA | CGGTAATAAA | 900 |
| AAATACGATA | TAGATGAATA | ACAAAACAGT | GAAGCAATCC | GTAACGATGG | 950 |
| TTGCTTCACT | GTTTTATTAT | GAATTATTAA | TAAGTGCTGT | TACTTCTCCC | 1000 |
| TTAAATACAA | TTTCTTCATT | TTCATTGTAT | GTTGAAAGTG | AACTGTAAAC | 1050 |
| GAGTCCATTT | TCTTTTTTTA | TGGATTTCTT | ATTTGTAAAT | TCAGCGATAA | 1100 |
| CGTACAATGT | ATTACCTGGG | TATACAGGTT | TAATAAATTT | AACGTTATTC | 1150 |
| ATTTGTGTTC | CTGCTACAAC | TTCTTCTCCG | TATTTACCTT | CTTCTACCCA | 1200 |
| TAATTTAAAT | GATATTGAAA | GTGTATGCAT | GCCAGATGCA | ATGATACCTT | 1250 |
| TAAATCTACT | TTGTTCTGCT | TTTTCTTTAT | CTATATGCAT | ATATTGAGGA | 1300 |
| TCAAAAGTTG | TTGCAAATTG | GATAATTTCT | TCTTCTGTAA | TATGAAGGCT | 1350 |
| TTTTGTTTTG | AATGTTTCTC | CTACTATAAA | ATCATCGTAT | TTCATATATG | 1400 |
| TCTCTCTTTC | TTATTCAAAT | TAATTTTTTA | GTATGTAACA | TGTTAAAGGT | 1450 |
| AAGTCTACCG | TCACTGAAAC | GTAAGACTCA | CCTCTAACTT | TCTATTGAGA | 1500 |

| | | | | | |
|-------------|-------------|-------------|------------|-------------|------|
| CAAATGCACC | ATTTTATCTG | CATTGTCTGT | AAAGATACCA | TCAACTCCCC | 1550 |
| AATTAGCAAG | TTGGTTTGCA | CGTGCTGGTT | TGTTTACAGT | CCATACGTTC | 1600 |
| AATTCATAAC | CCGCTTCTTT | TACCATTTTT | ACTTTTGCTT | TAGTAAGTTT | 1650 |
| GGCATCTTCA | GTGTTTACTA | TTTTAGCATT | ACAGTAATCT | AAAAGTGTTC | 1700 |
| TCCAGTCTTC | ACGAAACGAA | GTTGTATGGA | ATATAACTGC | TCTGTTATAT | 1750 |
| TGTGGCATGA | TTTCTTCTGC | AAGTTTAACA | AGCACACAT | TAAAGCTTGA | 1800 |
| AATGAGCACT | TCTTGATTCT | GATTTAAGTT | TGTTAATTGT | TCTTCCACTT | 1850 |
| GCTTAACCAT | ACTTTTAGAA | AGTGCTAGTC | CATTGCGTCC | AGTAATACCT | 1900 |
| TTTAATTCTA | CATTTAAATT | CATATTATAT | TCATTTGCTA | TTTTTACTAC | 1950 |
| ATCATCGAAA | GTTGGCAAAT | GTTTCATCTT | GAATTTTTC | CCAAACCAAG | 2000 |
| ATCCTGCAGA | AGCATCTTTA | ATTTTCATCAT | AATTCAATTC | AGTTATTTCC | 2050 |
| CCGGACATAT | TTGTAGTCCG | TTCTAAATAA | TCATCATGAA | TGATAATCAG | 2100 |
| TTGTTTCATCT | TTTGTAATTG | CAACATCTAA | CTCCAACCAG | TTTATACCTT | 2150 |
| CTACTTCTGA | AGCAGCTTTA | AATGATGCAA | TTGTATTTTC | CGGAGCTTTA | 2200 |
| CTAGGTAATC | CTCTATGTCC | ATATACAGTT | AGCATATTAC | CTCTCCTTGC | 2250 |
| ATTTTTATTT | TTTTAATTAA | CGTAACTGTA | TTATCACATT | AATCGCACTT | 2300 |
| TTATTTCCAT | TAAAAAGAGA | TGAATATCAT | AAATAAAGAA | GTCGATAGAT | 2350 |
| TCGTATTGAT | TATGGAGTTA | ATCTACGTCT | CATCTCATTT | TTAAAAAATC | 2400 |
| ATTTATGTCC | CAAGCTCCAT | TTTGTAATCA | AGTCTAGTTT | TTCTGTACCC | 2450 |
| CTTATCTGCA | ATTTTACTTA | GGATTGCTTT | TAACCTACCC | CTTATCAGCA | 2500 |
| ATTTTACTGA | GAACGTGCTTT | TAACGCACCT | CTTATCTGCA | ATTTTGCTTA | 2550 |
| GAACGTGCTTT | TAACGTACCT | CTTATCTGCA | ATTTTACTGA | GAACGTGCTTT | 2600 |
| TAACCTACCC | CTTATCAGCA | ATTTTGCATG | GAATTGCTTT | TAACGTACCT | 2650 |
| CTTATCTGCA | ATTTTACTTA | GAACGTGCTTT | TAACAAACCT | CTTATCTGCA | 2700 |
| ATTTTACTTA | GAACGTGCTTT | TAACGTACCT | CTTATCTGTA | ATTTTACTGA | 2750 |
| GAACGTGCTTT | TAACAAACCT | CTTATCTGCA | ATTTTACTTA | GAACGTGCTTT | 2800 |
| TAACAAACCT | CTTATCTGCA | ATTTTACTTA | GAATTGCTTT | TACTATTCCT | 2850 |
| CTTATTAGTA | TAATCTCAGT | AAGAATGCGT | ATAAAAATGA | AAATTACAAC | 2900 |
| CGATTTTGTA | AGTGCTGACG | CCTGAGGGAA | TAGTATGTGC | GAGAGACTAA | 2950 |
| TGGCTCGAGC | CATACCCCTA | GGCAAGCATG | CACGTACAAA | ATCGTAAGAT | 3000 |
| AAAAAAATAA | GCATATCACT | GTAAACTTTA | AAAAATCAGT | TTAGTGATAT | 3050 |
| GCTTATTTAT | TTCGAGTTAG | GATTTATGTC | CCAAGCTCAT | CAAGCACAAT | 3100 |
| CGGCCACTAG | TTTATTTCTC | TATCTTATAT | GTTCTGATAT | GGTCTTCTAT | 3150 |
| ACTGTATAAG | TATACTTTTG | AATATGGATC | TTGTGTCAAT | TCACGTTCGA | 3200 |
| AATCAAATTC | TTGATTATCA | AATCTGTAA | AGAATGTTTC | GTATTCTTCG | 3250 |
| ACTGATAATT | GCTCTCTAGA | TTCTAGCATA | TTTAAGTGTT | TCTCTTTATC | 3300 |
| TAATGCTTTG | TCATATCCTT | TAACGATTGA | ACCACTAAAG | ATTTCTCCTA | 3350 |
| CTGCTCCTGA | ACCATAACTA | AATAGACATA | CTTTCTCTTC | TGGTTGGAAT | 3400 |
| GTGTGGTTCT | GTAATAACGA | AATTAACTT | AAGTATAATG | ATCCTGTATA | 3450 |
| AATGTTACCA | ACATCTCTAT | TCCATAATAC | GGTTCTGTTG | CAAAGTTGAA | 3500 |
| TTTATA | | | | | 3506 |

2) INFORMATION FOR SEQ ID NO: 197

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(B) STRAIN: CCRI-175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197

| | | | | | |
|------------|------------|------------|------------|-------------|-----|
| TACATTAGAA | ATACAAGGAA | AGATGCTATC | TTCCGAAGGA | TTGGCCCAAG | 50 |
| AATTGAACCA | ACGCATGACC | CAAGGGCAAA | GCGACTTTGT | ATTTCGTCATT | 100 |
| GGCGGATCAA | ACGGCCTGCA | CAAGGACGTC | TTACAACGCA | GTAACCTACGC | 150 |
| ACTATCATTC | AGCAAAATGA | CATTCCCACA | TCAAATGATG | CGGGTTGTGT | 200 |
| TAATTGAACA | AGTGTAACAG | GCATTTAAGA | TTATGCGTGG | AGAAGCATAT | 250 |
| CATAAATGAT | GCGGTTTTTT | CAGCCGCTTC | ATAAAGGGAT | TTTGAATGTA | 300 |
| TCAGAACATA | TGAGGTTTAT | GTGAATTGCT | GTTATGTTTT | TAAGAAGCTT | 350 |
| ATCATAAGTA | ATGAGGTTCA | TGATTTTTGA | CATAGTTAGC | CTCCGCAGTC | 400 |
| TTTCATTTCA | AGTAAATAAT | AGCGAAATAT | TCTTTATACT | GAATACTTAT | 450 |
| AGTGAAGCAA | AGTTCTAGCT | TTGAGAAAAT | TCTTCTGCA | ACTAAATATA | 500 |
| GTAAATTACG | GTAAAATATA | AATAAGTACA | TATTGAAGAA | AATGAGACAT | 550 |
| AATATATTTT | ATAATAGGAG | GGAATTTCAA | ATGATAGACA | ACTTTATGCA | 600 |
| GGTCCTTAAA | TTAATTAAAG | AGAAACGTAC | CAATAATGTA | GTTAAAAAAT | 650 |
| CTGATTGGGA | TAAAGGTGAT | CTATATAAAA | CTTTAGTCCA | TGATAAGTTA | 700 |
| CCCAAGCAGT | TAAAAGTGCA | TATAAAAGAA | GATAAATATT | CAGTTGTAGG | 750 |
| GAAGGTTGCT | ACTGGGAACT | ATAGTAAAGT | TCCTTGGATT | TCAATATATG | 800 |
| ATGAGAATAT | AACAAAAGAA | ACAAAGGATG | GATATTATTT | GGTATATCTT | 850 |
| TTTCATCCGG | AAGGAGAAGG | CATATACTTA | TCTTTGAATC | AAGGATGGTC | 900 |
| AAAGATAAGT | GATATGTTTC | CGCGGGAT | | | 928 |

2) INFORMATION FOR SEQ ID NO: 198

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-1262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| CAATGCCCAC | AGAGTTATCC | ACAAATACAC | AGGTTATACA | CTAAAAATTG | 50 |
| GGCATGAATG | TCAGAAAAAT | ATCAAAAAC | GCAAAGAATA | TTGGTATAAT | 100 |
| AAGAGGGAAC | AGTGTGAACA | AGTTAATAAC | TTGTGGATAA | CTGGAAAGTT | 150 |
| GATAACAATT | TGGAGGACCA | AACGACATGA | AAATCACCAT | TTTAGCTGTA | 200 |
| GGGAAACTAA | AAGAGAAATA | TTGGAAGCAA | GCCATAGCAG | AATATGAAAA | 250 |
| ACGTTTAGGC | CCATACACCA | AGATAGACAT | CATAGAAGTT | CCAGACGAAA | 300 |
| AAGCACCAGA | AAATATGAGC | GACAAAGAAA | TTGAGCAAGT | AAAAGAAAAA | 350 |
| GAAGGCCAAC | GAATACTAGC | CAAAATCAAA | CCACAATCAA | CAGTCATTAC | 400 |
| ATTAGAAATA | CAAGGAAAGA | TGCTATCTTC | CGAAGGATTG | GCCCAAGAAT | 450 |
| TGAACCAACG | CATGACCCAA | GGGCAAAGCG | ACTTTGTATT | CGTCATTGGC | 500 |
| GGATCAAACG | GCCTGCACAA | GGACGTCTTA | CAACGCAGTA | ACTACGCACT | 550 |
| ATCATTCAGC | AAAATGACAT | TCCCACATCA | AATGATGCGG | GTTGTGTTAA | 600 |
| TTGAACAAGT | GTACAGAGCA | TTTAAGATTA | TGCGTGGAGA | AGCGTATCAT | 650 |
| AAATAAACT | AAAAATTAGG | TTGTGTATAA | TTTAAAAATT | TAATGAGATG | 700 |

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TGGAGGAATT | ACATATATGA | AATATTGGAT | TATACCTTGC | AATATCATAC | 750 |
| GATGTTTATA | GAGTGTTTAA | TAAACCATTT | TT | | 782 |

2) INFORMATION FOR SEQ ID NO: 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 709 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-8894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199

| | | | | | |
|------------|-------------|-------------|------------|-------------|-----|
| TACATTAGAA | ATACAAGGAA | AGATGCTATC | TTCCGAAGGA | TTGGCCCAAG | 50 |
| AATTGAACCA | ACGCATGACC | CAAGGGCAAA | GCGACTTTGT | TTTCGTCATT | 100 |
| GGCGGATCAA | ACGGCCTGCA | CAAGGACGTC | TTACAACGCA | GTAACCTACGC | 150 |
| ACTATCATTC | AGCAAAATGA | CATTCCCACA | TCAAATGATG | CGGGTTGTGT | 200 |
| TAATTGAACA | AGTGTAACAG | GCATTTAAGA | TTATGCGAGG | AGAAGCTTAT | 250 |
| CATAAGTAAT | GAGGTTTCATG | ATTTTTTGACA | TAGTTAGCCT | CCGCAGTCTT | 300 |
| TCATTTCAAG | TAAATAATAG | CGAAATATTC | TTTATACTGA | ATACTTATAG | 350 |
| TGAAGCAAAG | TTCTAGCTTT | GAGAAAATTC | TTTCTGCAAC | TAAATATAGT | 400 |
| AAATTACGGT | AAAATATAAA | TAAGTACATA | TTGAAGAAAA | TGAGACATAA | 450 |
| TATATTTTAT | AATAGGAGGG | AATTTCAAAT | GATAGACAAC | TTTATGCAGG | 500 |
| TCCTTAAATT | AATTAAAGAG | AAACGTACCA | ATAATGTAGT | TAAAAAATCT | 550 |
| GATTGGGATA | AAGGTGATCT | ATATAAAACT | TTAGTCCATG | ATAAGTTACC | 600 |
| CAAGCAGTTA | AAAGTGCATA | TAAAAGAAGA | TAAATATTCA | GTTGTAGGGA | 650 |
| AGGTTGCTAC | TGGGAACAT | AGTAAAGTTC | CTTGGATTTC | AATATATGAT | 700 |
| GAGAATATA | | | | | 709 |

2) INFORMATION FOR SEQ ID NO: 200

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200

GTGGGAAATG GCTGTTGTTG AG

22

2) INFORMATION FOR SEQ ID NO: 201

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201

TTCGTTCCCT CCATTAAGTG TC

22

2) INFORMATION FOR SEQ ID NO: 202

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202

AAAAGAAAGA CGGTGAAGGC

20

2) INFORMATION FOR SEQ ID NO: 203

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203

CACTTCATTA TACTGTTTTT TTTGC

25

2) INFORMATION FOR SEQ ID NO: 204

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204

TCACCGTCTT TCTTTTGACC TT

22

2) INFORMATION FOR SEQ ID NO: 205

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205

TGAGATCTGC TGGAACAAAA GTGAA

25

2) INFORMATION FOR SEQ ID NO: 206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206

CGGTCGAGTT TGCTGAAGAA

20

2) INFORMATION FOR SEQ ID NO: 207

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207

TCCCCTAATG ATAGCTGGTA TATATT

26

2) INFORMATION FOR SEQ ID NO: 208

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208

TCTAGGGAAT CAAAGAAAAG TAATAGT

27

2) INFORMATION FOR SEQ ID NO: 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209

CAACAARGRC AATGTGAYRT ATTATGYTGT TA

32

2) INFORMATION FOR SEQ ID NO: 210

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210

GATAAYATWG GMGAACAAGT CARAAATGG

29

2) INFORMATION FOR SEQ ID NO: 211

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211

CCRTATTGAT TGWTRACACG RCCACARTAA TTWGG

35

2) INFORMATION FOR SEQ ID NO: 212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212

ATRTTSARTG GTTCATTTTTT GAAATAGATI CC

32

2) INFORMATION FOR SEQ ID NO: 213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213

ACGTGTCGGT ATCTATGTWC GTGTATCAAC RG

32

2) INFORMATION FOR SEQ ID NO: 214

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214

TGTTATGRTC TACAAAACAA ACCGAYTAGC

30

2) INFORMATION FOR SEQ ID NO: 215

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215

GAWTAATAAT RGGGGAATGC TTACCTTCAG CTAT

34

2) INFORMATION FOR SEQ ID NO: 216

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 bases
 - (B) TYPE: Nucleic acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216

GGTTTTTGAC TGACTTGTTT TTTACG

26

2) INFORMATION FOR SEQ ID NO: 217

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 bases

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217

TAGAAYTGTT TTTTATGATT ACCRTCTTT

29

2) INFORMATION FOR SEQ ID NO: 218

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218

GGCAAAAAYA AAGACGAAGT GCTGAG

26

2) INFORMATION FOR SEQ ID NO: 219

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 721 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TGTAGCTTTA | GGTGAAGGGT | TAGGTCCTTC | AATAGGGGGA | ATAATAGCAC | 50 |
| ATTATATTCA | TTGGTCTTAC | CTACTTATAC | TTCCTATGAT | TACAATAGTA | 100 |
| ACTATACCTT | TTCTTATTAA | AGTAATGGTA | CCTGGTAAAT | CAACAAAAAA | 150 |
| TACATTAGAT | ATCGTAGGTA | TTGTTTTAAT | GTCTATAAGT | ATTATATGTT | 200 |
| TTATGTTATT | TACGACAAAT | TATAATTGGA | CTTTTTTAAT | ACTCTTCACA | 250 |
| ATCTTTTTTG | TGATTTTTAT | TAAACATATT | TCAAGAGTTT | CTAACCCTTT | 300 |
| TATTAATCCT | AAACTAGGGA | AAAACATTCC | GTTTATGCTT | GGTTTGTTTT | 350 |
| CTGGTGGGCT | AATATTTTCT | ATAGTAGCTG | GTTTTATATC | AATGGTGCCT | 400 |
| TATATGATGA | AAACTATTTA | TCATGTAAAT | GTAGCGACAA | TAGGTAATAG | 450 |

| | | | | | |
|-------------|------------|------------|-------------|------------|-----|
| TGTTATTTTT | CCTGGAACCA | TGAGTGTTAT | TGTTTTTTGGT | TATTTTGGTG | 500 |
| GTTTTTTTAGT | GGATAGAAAA | GGATCATTAT | TTGTTTTTTAT | TTTAGGATCA | 550 |
| TTGTCTATCT | CTATAAGTTT | TTTAACTATT | GCATTTTTTTG | TTGAGTTTAG | 600 |
| TATGTGGTTG | ACTACTTTTA | TGTTTATATT | TGTTATGGGC | GGATTATCTT | 650 |
| TTACTAAAAC | AGTTATATCA | AAAATAGTAT | CAAGTAGTCT | TTCTGAAGAA | 700 |
| GAAGTTGCTT | CTGGAAGAGT | T | | | 721 |

2) INFORMATION FOR SEQ ID NO: 220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1791 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-1331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220

| | | | | | |
|------------|-------------|-------------|------------|------------|------|
| ATCCGGTACT | GCAGAACTCA | AAATGAAACA | AGGAGAAACT | GGCAGACAAA | 50 |
| TTGGGTGGTT | TATATCATAT | GATAAAGATA | ATCCAAACAT | GATGATGGCT | 100 |
| ATTAATGTTA | AAGATGTACA | AGATAAAGGA | ATGGCTAGCT | ACAATGCCAA | 150 |
| AATCTCAGGT | AAAGTGTATG | ATGAGCTATA | TGAGAACGGT | AATAAAAAAT | 200 |
| ACGATATAGA | TGAATAACAA | AACAGTGAAG | CAATCCGTAA | CGATGGTTGC | 250 |
| TTCACTGTTT | TATTATGAAT | TATTAATAAG | TGCTGTTACT | TCTCCCTTAA | 300 |
| ATACAATTTT | TTCAATTTTCA | TTGTATGTTG | AAAGTGACAC | TGTAACGAGT | 350 |
| CCATTTTCTT | TTTTTATGGA | TTTCTTATTT | GTAATTTTCA | CGATAACGTA | 400 |
| CAATGTATTA | CCTGGGTATA | CAGGTTTAAAT | AAATTTAACG | TTATTCATTT | 450 |
| GTGTTCCCTG | TACAACCTTCT | TCTCCGTATT | TACCTTCTTC | TACCCATAAT | 500 |
| TTAAATGATA | TTGAAAGTGT | ATGCATGCCA | GATGCAATGA | TACCTTTAAA | 550 |
| TCTACTTTGT | TCTGCTTTTT | CTTTATCTAT | ATGCATATAT | TGAGGATCAA | 600 |
| AAGTTGTTGC | AAATTGGATA | ATTTCTTCTT | CTGTAATATG | AAGGCTTTTT | 650 |
| GTTTTGAATG | TTTCTCCTAC | TATAAAATCA | TCGTATTTCA | TATATGTCTC | 700 |
| TCTTTCTTAT | TCAAATTAAT | TTTTTTAGTAT | GTAACATGTT | AAAGGTAAGT | 750 |
| CTACCGTCAC | TGAAACGTAA | GACTCACCTC | TAACCTTCTA | TTGAGACAAA | 800 |
| TGCACCATTT | TATCTGCATT | GTCTGTAAAG | ATACCATCAA | CTCCCCAATT | 850 |
| AGCAAGTTGG | TTTGACAGTG | CTGGTTTGTT | TACAGTCCAT | ACGTTCAATT | 900 |
| CATAACCCGC | TTCTTTTACC | ATTTTTACTT | TTGCTTTAGT | AAGTTTGGCA | 950 |
| TCTTCAGTGT | TTACTATTTT | AGCATTACAG | TAATCTAAAA | GTGTTCTCCA | 1000 |
| GTCTTCACGA | AACGAAGTTG | TATGGAATAT | AACTGCTCTG | TTATATTGTG | 1050 |
| GCATGATTTT | TTCTGCAAGT | TTAACAAGCA | CAACATTAAA | GCTTGAAATG | 1100 |
| AGCACTTCTT | GATTCTGATT | TAAGTTTGTT | AATTGTTCTT | CCACTTGCTT | 1150 |
| AACCATACTT | TTAGAAAGTG | CTAGTCCATT | CGGTCCAGTA | ATACCTTTTA | 1200 |
| ATTCTACATT | TAAATTCATA | TTATATTCAAT | TTGCTATTTT | TACTACATCA | 1250 |
| TCGAAAGTTG | GCAAATGTTC | ATCTTTGAAT | TTTTCACCAA | ACCAAGATCC | 1300 |
| TGCAGAAGCA | TCTTTAATTT | CATCATAATT | CAATTCAGTT | ATTTCCCCGG | 1350 |
| ACATATTTGT | AGTCCGTTCT | AAATAATCAT | CATGAATGAT | AATCAGTTGT | 1400 |
| TCATCTTTTG | TAATTGCAAC | ATCTAACTCC | AACCAGTTTA | TACCTTCTAC | 1450 |
| TTCTGAAGCA | GCTTTAAATG | ATGCAATTGT | ATTTTCCGGA | GCTTTACTAG | 1500 |
| GTAATCCTCT | ATGTCCATAT | ACAGTTAGCA | TATTACCTCT | CCTTGCATTT | 1550 |
| TTATTTTTTT | AATTAACGTA | ACTGTATTAT | CACATTAATC | GCACTTTTAT | 1600 |

| | | | | | |
|------------|------------|-------------|------------|-------------|------|
| TTCCATTAAA | AAGAGATGAA | TATCATAAAT | AAAGAAGTCG | ATAGATTTCGT | 1650 |
| ATTGATTATG | GAGTTAATCT | ACGTCTCATC | TCATTTTAA | AAAATCATT | 1700 |
| ATGTCCAAG | CTCCATTTTG | TAATCAAGTC | TAGTTTTTCT | GTACCCCTTA | 1750 |
| TCTGCAATTT | TACTTAGGAT | TGCTTTTAAAC | TTACCCCTTA | T | 1791 |

2) INFORMATION FOR SEQ ID NO: 221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| AAGTGCTGAC | GCCTGAGGGA | ATAGTATGTG | CGAGAGACTA | ATGGCTCGAG | 50 |
| CCATACCCCT | AGGCAAGCAT | GCACGTACAA | AATCGTAAGA | TAAAAAATA | 100 |
| AGCATATCAC | TGTAAACTTT | AAAAAATCAG | TTAGTGATA | TGCTTATTTA | 150 |
| TTTCGAGTTA | GGATTTATGT | CCCAAGCTCA | TCAAGCACAA | TCGGCCACTA | 200 |
| GTTTATTTCT | CTATCTTATA | TGTTCTGATA | TGGTCTTCTA | TACTGTATAA | 250 |
| GTATACTTTT | GAATATGGAT | CTTGTGTCAA | TTCACGTTTC | AAATCAAATT | 300 |
| CTTGATTATC | AAATCTGTTA | AAGAATGTTT | CGTATTCTTC | GACTGATAAT | 350 |
| TGCTCTCTAG | ATTCTAGCAT | ATTTAAGTGT | TTCTCTTTAT | CTAATGCTTT | 400 |
| GTCATATCCT | TTAACGATTG | AACCACTAAA | GATTTCCTCT | ACTGCTCCTG | 450 |
| AACCATAACT | AAATAGACAT | ACTTCTCTCT | CTGGTTGGAA | TGTGTGGTTC | 500 |
| TGTAATAACG | AAATTAAACT | TAAGTATAAT | GATCCTGTAT | AAATGTTACC | 550 |
| AACATCTCTA | TTCCATAATA | CGGTTCTGTT | GCAAAGTTGA | ATTTATAGTA | 600 |

2) INFORMATION FOR SEQ ID NO: 222

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222

| | | | | | |
|-------------|-------------|------------|-------------|------------|------|
| GGGTGGTTTA | TATCATATGA | TAAAGATAAT | CCAAACATGA | TGATGGCTAT | 50 |
| TAATGTTAAA | GATGTACAAG | ATAAAGGAAT | GGCTAGCTAC | AATGCCAAAA | 100 |
| TCTCAGGTAA | AGTGTATGAT | GAGCTATATG | AGAACGGTAA | TAAAAAATAC | 150 |
| GATATAGATG | AATAACAAAA | CAGTGAAGCA | ATCCGTAACG | ATGGTTGCTT | 200 |
| CACTGTTTTA | TTATGAATTA | TTAATAAGTG | CTGTTACTTC | TCCCTTAAAT | 250 |
| ACAATTTCTT | CATTTTCATT | GTATGTTGAA | AGTGACACTG | TAACGAGTCC | 300 |
| ATTTTCTTTT | TTTATGGATT | TCTTATTTGT | AATTTTCAGCG | ATAACGTACA | 350 |
| ATGTATTACC | TGGGTATACA | GGTTTAATAA | ATTTAACGTT | ATTCATTTGT | 400 |
| GTTCCTGCTA | CAACTTCTTC | TCCGTATTTA | CCTTCTTCTA | CCCATAATTT | 450 |
| AAATGATATT | GAAAGTGTAT | GCATGCCAGA | TGCAATGATA | CCTTTAAATC | 500 |
| TACTTTGTTC | TGCTTTTTCT | TTATCTATAT | GCATATATTG | AGGATCAAAA | 550 |
| GTTGTTGCAA | ATTGGATAAT | TTCTTCTTCT | GTAATATGAA | GGCTTTTTGT | 600 |
| TTTGAATGTT | TCTCCTACTA | TAAAATCATC | GTATTTCATA | TATGTCTCTC | 650 |
| TTTCTTATTC | AAATTAATTT | TTTAGTATGT | AACATGTTAA | AGGTAAGTCT | 700 |
| ACCGTCACTG | AAACGTAAGA | CTCACCTCTA | ACTTTCTATT | GAGACAAATG | 750 |
| CACCATTTTA | TCTGCATTGT | CTGTAAAGAT | ACCATCAACT | CCCCAATTAG | 800 |
| CAAGTTGGTT | TGCACGTGCT | GGTTTGTTTA | CAGTCCATAC | GTTCAATTCA | 850 |
| TAACCCGCTT | CTTTTACCAT | TTTTACTTTT | GCTTTAGTAA | GTTTGGCATC | 900 |
| TTCAGTGTTT | ACTATTTTAG | CATTACAGTA | ATCTAAAAGT | GTTCTCCAGT | 950 |
| CTTCACGAAA | CGAAGTTGTA | TGGAATATAA | CTGCTCTGTT | ATATTGTGGC | 1000 |
| ATGATTTCTT | CTGCAAGTTT | AACAAGCACA | ACATTAAAGC | TTGAAATGAG | 1050 |
| CACTTCTTGA | TTCTGATTTA | AGTTTGTTAA | TTGTTCTTCC | ACTTGCTTAA | 1100 |
| CCATACTTTT | AGAAAGTGCT | AGTCCATTCT | GTCCAGTAAT | ACCTTTTAAT | 1150 |
| TCTACATTTA | AATTCATATT | ATATTCATTT | GCTATTTTTA | CTACATCATC | 1200 |
| GAAAGTTGGC | AAATGTTTCAT | CTTTGAATTT | TTCACCAAAC | CAAGATCCTG | 1250 |
| CAGAAGCATC | TTTAATTTCA | TCATAATTCA | ATTCAGTTAT | TTCCCCGGAC | 1300 |
| ATATTTGTAG | TCCGTTCTAA | ATAATCATCA | TGAATGATAA | TCAGTTGTTC | 1350 |
| ATCTTTTGTA | ATTGCAACAT | CTAACTCCAA | CCAGTTTATA | CCTTCTACTT | 1400 |
| CTGAAGCAGC | TTTAAATGAT | GCAATTGTAT | TTTCCGGAGC | TTTACTAGGT | 1450 |
| AATCCTCTAT | GTCCATATAC | AGTTAGCATA | TTACCTCTCC | TTGCATTTTT | 1500 |
| ATTTTTTTTAA | TTAACGTAAC | TGTATTATCA | CATTAATCGC | ACTTTTATTT | 1550 |
| CCATTAAAAA | GAGATGAATA | TCATAAATAA | AGAAGTCGAT | AGATTCGTAT | 1600 |
| TGATTATGGA | GTTAATCTAC | GTCTCATCTC | ATTTTTAAAA | | 1640 |

2) INFORMATION FOR SEQ ID NO: 223

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-2025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223

| | | | | | |
|------------|------------|------------|------------|-------------|-----|
| AATTCAACTT | TGCAACAGAA | CCGTATTATG | GAATAGAGAT | GTTGGTAACA | 50 |
| TTTATACAGG | ATCATTATAC | TTAAGTTTAA | TTTCGTTATT | ACAGAACCAC | 100 |
| ACATTCCAAC | CAGAAGAGAA | AGTATGTCTA | TTTAGTTATG | G TTCAGGAGC | 150 |
| AGTAGGAGAA | ATCTTTAGTG | GTTCAATCGT | TAAAGGATAT | GACAAAGCAT | 200 |
| TAGATAAAGA | GAAACACTTA | AATATGCTAG | AATCTAGAGA | GCAATTATCA | 250 |

| | | | | | |
|------------|------------|------------|-------------|------------|-----|
| GTCGAAGAAT | ACGAAACATT | CTTTAACAGA | TTTGATAATC | AAGAATTTGA | 300 |
| TTTCGAACGT | GAATTGACAC | AAGATCCATA | TTCAAAAAGTA | TACTTATACA | 350 |
| GTATAGAAGA | CCATATCAGA | ACATATAAGA | TAGAGAAATA | AACTAGTGGC | 400 |
| CGATTGTGCT | TGATGAGCTT | GGGACATAAA | TCCTAACTCG | AAATAAATAA | 450 |
| GCATATCACT | AAACTGATTT | TTTAAAGTTT | ACAGTGATAT | GCTTATTTTT | 500 |
| TTATCTTACG | ATTTTGTACG | TGCATGCTTG | CCTAGGGGTA | TGGCTCGAGC | 550 |
| CATTAGTCTC | TCGCACATAC | TATTCCCTCA | GGCGTCAGCA | CT | 592 |

2) INFORMATION FOR SEQ ID NO: 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2386 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224

| | | | | | |
|------------|-------------|-------------|------------|------------|------|
| CACCTTCATA | TGACGTCTAT | CCATTTATGT | ATGGCATGAG | TAACGAAGAA | 50 |
| TATAATAAAT | TAACCGAAGA | TAAAAAAGAA | CCTCTGCTCA | ACAAGTTCCA | 100 |
| GATTACAAC | TCACCAGGTT | CAACTCAAAA | AATATTAACA | GCAATGATTG | 150 |
| GGTTAAATAA | CAAAACATTA | GACGATAAAA | CAAGTTATAA | AATCGATGGT | 200 |
| AAAGGTTGGC | AAAAAGATAA | ATCTTGGGGT | GGTTACAACG | TTACAAGATA | 250 |
| TGAAGTGGTA | AATGGTAATA | TCGACTTAAA | ACAAGCAATA | GAATCATCAG | 300 |
| ATAACATTTT | CTTTGCTAGA | GTAGCACTCG | AATTAGGCAG | TAAGAAATTT | 350 |
| GAAAAAGGCA | TGAAAAAACT | AGGTGTTGGT | GAAGATATAC | CAAGTGATTA | 400 |
| TCCATTTTAT | AATGCTCAAA | TTTCAAACAA | AAATTTAGAT | AATGAAATAT | 450 |
| TATTAGCTGA | TTCAGGTTAC | GGACAAGGTG | AAATACTGAT | TAACCCAGTA | 500 |
| CAGATCCTTT | CAATCTATAG | CGCATTAGAA | AATAATGGCA | ATATTAACGC | 550 |
| ACCTCACTTA | TTAAAAGACA | CGAAAAACAA | AGTTTGGAAG | AAAAATATTA | 600 |
| TTTCCAAAGA | AAATATCAAT | CTATTAAGTG | ATGGTATGCA | ACAAGTCGTA | 650 |
| AATAAAACAC | ATAAAGAAGA | TATTTATAGA | TCTTATGCAA | ACTTAATTGG | 700 |
| CAAATCCGGT | ACTGCAGAAC | TCAAAATGAA | ACAAGGAGAA | ACTGGCAGAC | 750 |
| AAATTGGGTG | GTTTATATCA | TATGATAAAG | ATAATCCAAA | CATGATGATG | 800 |
| GCTATTAATG | TTAAAGATGT | ACAAGATAAA | GGAATGGCTA | GCTACAATGC | 850 |
| CAAAATCTCA | GGTAAAGTGT | ATGATGAGCT | ATATGAGAAC | GGTAATAAAA | 900 |
| AATACGATAT | AGATGAATAA | CAAAACAGTG | AAGCAATCCG | TAACGATGGT | 950 |
| TGCTTCACTG | TTTTATTATG | AATTATTAAT | AAGTGCTGTT | ACTTCTCCCT | 1000 |
| TAAATACAAT | TTCTTCATTT | TCATTGTATG | TTGAAAGTGA | CACTGTAACG | 1050 |
| AGTCCATTTT | CTTTTTTTTAT | GGATTTCTTA | TTTGTAATTT | CAGCGATAAC | 1100 |
| GTACAATGTA | TTACCTGGGT | ATACAGGTTT | AATAAATTTA | ACGTTATTCA | 1150 |
| TTTGTGTTCC | TGCTACAAC | TCTTCTCCGT | ATTTACCTTC | TTCTACCCAT | 1200 |
| AATTTAAATG | ATATTGAAAG | TGTATGCATG | CCAGATGCAA | TGATACCTTT | 1250 |
| AAATCTACTT | TGTTCTGCTT | TTTCTTTATC | TATATGCATA | TATTGAGGAT | 1300 |
| CAAAAGTTGT | TGCAAATTGG | ATAATTTCTT | CTTCTGTAAT | ATGAAGGCTT | 1350 |
| TTTGTTTTGA | ATGTTTCTCC | TACTATAAAA | TCATCGTATT | TCATATATGT | 1400 |
| CTCTCTTTCT | TATTCAAATT | AATTTTTTTAG | TATGTAACAT | GTAAAGGTA | 1450 |
| AGTCTACCGT | CACTGAAACG | TAAGACTCAC | CTCTAACTTT | CTATTGAGAC | 1500 |
| AAATGCACCA | TTTTATCTGC | ATTGTCTGTA | AAGATACCAT | CAACTCCCCA | 1550 |

| | | | | | |
|-------------|------------|------------|-------------|------------|------|
| ATTAGCAAGT | TGGTTTGCAC | GTGCTGGTTT | GTTTACAGTC | CATACGTTCA | 1600 |
| ATTCATAACC | CGCTTCTTTT | ACCATTTTTA | CTTTTGCTTT | AGTAAGTTTG | 1650 |
| GCATCTTCAG | TGTTTACTAT | TTTAGCATTA | CAGTAATCTA | AAAGTGTTCT | 1700 |
| CCAGTCTTCA | CGAAACGAAG | TTGTATGGAA | TATAACTGCT | CTGTTATATT | 1750 |
| GTGGCATGAT | TTCTTCTGCA | AGTTTAACAA | GCACAACATT | AAAGCTTGAA | 1800 |
| ATGAGCACTT | CTTGATTCTG | ATTTAAGTTT | GTTAATTGTT | CTTCCACTTG | 1850 |
| CTTAACCATA | CTTTTAGAAA | GTGCTAGTCC | ATTCGGTCCA | GTAATACCTT | 1900 |
| TTAATTCTAC | ATTTAAATTC | ATATTATATT | CATTTGCTAT | TTTTACTACA | 1950 |
| TCATCGAAAG | TTGGCAAATG | TTCATCTTTG | AATTTTTCAC | CAAACCAAGA | 2000 |
| TCCTGCAGAA | GCATCTTTAA | TTTCATCATA | ATTCAATTCA | GTTATTTCCC | 2050 |
| CGGACATATT | TGTAGTCCGT | TCTAAATAAT | CATCATGAAT | GATAATCAGT | 2100 |
| TGTTTCATCTT | TTGTAATTGC | AACATCTAAC | TCCAACCAAGT | TTATACCTTC | 2150 |
| TACTTCTGAA | GCAGCTTTAA | ATGATGCAAT | TGTATTTTCC | GGAGCTTTAC | 2200 |
| TAGGTAATCC | TCTATGTCCA | TATACAGTTA | GCATATTACC | TCTCCTTGCA | 2250 |
| TTTTTATTTT | TTTAATTAAC | GTAAGTGTAT | TATCACATTA | ATCGCACTTT | 2300 |
| TATTTCCATT | AAAAAGAGAT | GAATATCATA | AATAAAGAAG | TCGATAGATT | 2350 |
| CGTATTGATT | ATGGAGTTAA | TCTACGTCTC | ATCTCA | | 2386 |

2) INFORMATION FOR SEQ ID NO: 225

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 623 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: CCRI-9860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225

| | | | | | |
|-------------|------------|-------------|------------|-------------|-----|
| TGAAAATTAC | AACCGATTTT | GTAAGTGCTG | ACGCCTGAGG | GAATAGTATG | 50 |
| TGCGAGAGAC | TAATGGCTCG | AGCCATACCC | CTAGGCAAGC | ATGCACGTAC | 100 |
| AAAATCGTAA | GATAAAAAAA | TAAGCATATC | ACTGTAAACT | TTAAAAAATC | 150 |
| AGTTTAGTGA | TATGCTTATT | TATTTTCGAGT | TAGGATTTAT | GTCCCAAGCT | 200 |
| CATCAAGCAC | AATCGGCCAC | TAGTTTATTT | CTCTATCTTA | TATGTTCTGA | 250 |
| TATGGTCTTC | TATACTGTAT | AAGTATACTT | TTGAATATGG | ATCTTGTTGTC | 300 |
| AATTCACGTT | CGAAATCAAA | TTCTTGATTA | TCAAATCTGT | TAAAGAATGT | 350 |
| TTCGTATTCT | TCGACTGATA | ATTGCTCTCT | AGATTCTAGC | ATATTTAAGT | 400 |
| GTTTCTCTTT | ATCTAATGCT | TTGTCATATC | CTTTAACGAT | TGAACCACTA | 450 |
| AAGATTTCCTC | CTACTGCTCC | TGAACCATAA | CTAAATAGAC | ATACTTTCTC | 500 |
| TTCTGGTTGG | AATGTGTGGT | TCTGTAATAA | CGAAATTAAA | CTTAAGTATA | 550 |
| ATGATCCTGT | ATAAATGTTA | CCAACATCTC | TATTCATATA | TACGGTTCTG | 600 |
| TTGCAAAGTT | GAATTTATAG | TAT | | | 623 |

2) INFORMATION FOR SEQ ID NO: 226

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 bases

- (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (C) ACCESSION NUMBER: Extracted from L29436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGAAAAATA | TTTCAGAATT | CTCAGCCCAA | CTTGATCAAA | CTTTTGATCA | 50 |
| AGGGGAAGCC | GTCTCTATGG | AGTGGTTATT | CCGTCCGTTG | CTAAAAATGC | 100 |
| TGGCGGAGGG | CGATCCAGTC | CCCGTTGAGG | ACATCGCGGC | GGAGACCGGG | 150 |
| AAGCCCGTCG | AGGAAGTTAA | GCAAGTCCTA | CAGACTCTAC | CTAGTGTGGA | 200 |
| ACTTGATGAG | CAGGGCCGTG | TCGTCCGTTA | TGGCCTCACA | CTGTTCCCTA | 250 |
| CCCCCATCG | CTTCGAGGTT | GATGGGAAGC | AACTATATGC | ATGGTGCGCC | 300 |
| CTTGACACAC | TTATGTTCCC | AGCACTCATC | GGCCGGACGG | TCCACATCGC | 350 |
| TTCGCCTTGT | CACGGCACCG | GTAAGTCCGT | CCGGTTGACG | GTGGAACCGG | 400 |
| ACCGCGTTGT | AAGCGTCGAG | CCTTCAACAG | CCGTTGTCTC | GATTGTTACA | 450 |
| CCAGATGAAA | TGGCCTCGGT | TCGGTCGGCC | TTCTGTAACG | ACGTTCACTT | 500 |
| TTTCAGTTCA | CCGAGTGCAG | CCCAAGACTG | GCTTAACCAA | CACCCTGAGT | 550 |
| CGAGCGTTTT | GCCCGTTGAA | GATGCCTTTG | AACTGGGTCG | CCATTTGGGA | 600 |
| GCGCGTTATG | AGGAGTCAGG | ACCTACTAAT | GGGTCCTGTT | GTAACATTTA | 650 |
| A | | | | | 651 |

2) INFORMATION FOR SEQ ID NO: 227

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
 (C) ACCESSION NUMBER: Extracted from L29436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227

| | | | | | |
|------------|------------|-------------|------------|------------|-----|
| ATGAATCTTG | AAAAAGGGAA | TATAGAAAGG | AAAAAACATG | GTGTCCATGT | 50 |
| TAATGAGTAT | TTGCAAAGTG | TAAGTAACCC | GAATGTCTAT | GCAGCTGGAG | 100 |
| ATGCTGCAGC | AACGGATGGC | TTGCCCCCTCA | CACCTGTAGC | CAGTGCAGAT | 150 |
| TCTCATGTCG | TAGCATCTAA | TTTATTGAAA | GGGAACAGCA | AAAAAATTGA | 200 |
| ATATCCCGTG | ATTCCATCTG | CTGTATTTAC | CGTACCTAAA | ATGGCATCGG | 250 |
| TAGGTATGAG | CGAGGAGGAA | GCCAAAAACT | CTGGCCGGAA | TATTAAAGTA | 300 |
| AAGCAGAAAA | ACATCTCCGA | CTGGTTTACG | TATAAACGGA | CAAATGAGGA | 350 |
| CTTTGCTGCG | TTTAAAGTGC | TGATTGACGA | AGATCATGAT | CAAATTGTTG | 400 |
| GTGCTCATTT | GATTAGTAAT | GAAGCCGATG | AACTGATTAA | TCATTTTGCA | 450 |
| ACAGCCATTC | GTTTTGGGAT | TTCAACCAAA | GAATTGAAAC | AAATGATATT | 500 |

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| TGCCTATCCA | ACGGCAGCTT | CGGACATTGC | ACACATGTTG | TAAGTTTGCG | 550 |
| TTTTGTGAGA | TGT | | | | 563 |

2) INFORMATION FOR SEQ ID NO: 228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1380 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (C) ACCESSION NUMBER: Extracted from S67449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228

| | | | | | |
|------------|------------|-------------|-------------|------------|------|
| TTGTTTAGTT | TATATAAAAA | ATTTAAAGGT | TTGTTTTATA | GCGTTTTATT | 50 |
| TTGGCTTTGT | ATTCTTTCAT | TTTTTAGTGT | ATTAAATGAA | ATGGTTTTAA | 100 |
| ATGTTTCTTT | ACCTGATATT | GCAAATCATT | TTAATACTAC | TCCTGGAATT | 150 |
| ACAAACTGGG | TAAACACTGC | ATATATGTTA | ACTTTTTTCGA | TAGGAACAGC | 200 |
| AGTATATGGA | AAATTATCTG | ATTATATAAA | TATAAAAAAA | TTGTTAATTA | 250 |
| TTGGTATTAG | TTTGAGCTGT | CTTGGTTCAT | TGATTGCTTT | TATTGGTCAC | 300 |
| AATCACTTTT | TTATTTTGAT | TTTTGGTAGG | TTAGTACAAG | GAGTAGGATC | 350 |
| TGCTGCATTC | CCTTCACTGA | TTATGGTGGT | TGTAGCTAGA | AATATTACAA | 400 |
| GAAAAAACA | AGGCAAAGCC | TTTGGTTTTA | TAGGATCAAT | TGTAGCTTTA | 450 |
| GGTGAAGGGT | TAGGTCCTTC | AATAGGGGGA | ATAATAGCAC | ATTATATTCA | 500 |
| TTGGTCTTAC | CTACTTATAC | TTCCTATGAT | TACAATAGTA | ACTATACCTT | 550 |
| TTCTTATTAA | AGTAATGGTA | CCTGGTAAAT | CAACAAAAAA | TACATTAGAT | 600 |
| ATCGTAGGTA | TTGTTTTAAT | GTCTATAAGT | ATTATATGTT | TTATGTTATT | 650 |
| TACGACAAAT | TATAATTGGA | CTTTTTTAAAT | ACTCTTCACA | ATCTTTTTTG | 700 |
| TGATTTTTAT | TAAACATATT | TCAAGAGTTT | CTAACCTTTT | TATTAATCCT | 750 |
| AAACTAGGGA | AAAACATTCC | GTTTATGCTT | GGTTTGTTTT | CTGGTGGGCT | 800 |
| AATATTTTCT | ATAGTAGCTG | GTTTTATATC | AATGGTGCCT | TATATGATGA | 850 |
| AAACTATTTA | TCATGTAAAT | GTAGCGACAA | TAGGTAATAG | TGTTATTTTT | 900 |
| CCTGGAACCA | TGAGTGTTAT | TGTTTTTGGT | TATTTTGGTG | GTTTTTTAGT | 950 |
| GGATAGAAAA | GGATCATTAT | TTGTTTTTAT | TTTAGGATCA | TTGTCTATCT | 1000 |
| CTATAAGTTT | TTTAACTATT | GCATTTTTTG | TTGAGTTTAG | TATGTGGTTG | 1050 |
| ACTACTTTTA | TGTTTATATT | TGTTATGGGC | GGATTATCTT | TTACTAAAAC | 1100 |
| AGTTATATCA | AAAATAGTAT | CAAGTAGTCT | TTCTGAAGAA | GAAGTTGCTT | 1150 |
| CTGGAATGAG | TTTGCTAAAT | TTCACAAGTT | TTTTATCAGA | GGGAACAGGT | 1200 |
| ATAGCAATTG | TAGGAGGTTT | ATTGTCACTA | CAATTGATTA | ATCGTAAACT | 1250 |
| AGTTCTGGAA | TTTATAAATT | ATTCTTCTGG | AGTGTATAGT | AATATTCTTG | 1300 |
| TAGCCATGGC | TATCCTTATT | ATTTTATGTT | GTCTTTTGAC | GATTATTGTA | 1350 |
| TTTAAACGTT | CTGAAAAGCA | GTTTGAATAG | | | 1380 |

2) INFORMATION FOR SEQ ID NO: 229

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 bases

119/125

- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: HUC19
- (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229

| | | | | | |
|-------------|------------|------------|------------|------------|------|
| ATGAGAATAG | TGAATGGACC | AATAATAATG | ACTAGAGAAG | AAAGAATGAA | 50 |
| GATTGTTTCAT | GAAATTAAGG | AACGAATATT | GGATAAATAT | GGGGATGATG | 100 |
| TTAAGGCTAT | TGGTGTTTAT | GGCTCTCTTG | GTCGTCAGAC | TGATGGGCCC | 150 |
| TATTCGGATA | TTGAGATGAT | GTGTGTCATG | TCAACAGAAG | AAGCAGAGTT | 200 |
| CAGCCATGAA | TGGACAACCG | GTGAGTGGAA | GGTGGAAGTG | AATTTTGATA | 250 |
| GCGAAGAGAT | TCTACTAGAT | TATGCATCTC | AGGTGGAATC | AGATTGGCCT | 300 |
| CTTACACATG | GTCAATTTTT | CTCTATTTTG | CCGATTTATG | ATTCAGGTGG | 350 |
| ATACTTAGAG | AAAGTGTATC | AAACTGCTAA | ATCGGTAGAA | GCCCAAACGT | 400 |
| TCCACGATGC | GATTTGTGCC | CTTATCGTAG | AAGAGCTGTT | TGAATATGCA | 450 |
| GGCAAATGGC | GTAATATTCG | TGTGCAAGGA | CCGACAACAT | TTCTACCATC | 500 |
| CTTGACTGTA | CAGGTAGCAA | TGGCAGGTGC | CATGTTGATT | GGTCTGCATC | 550 |
| ATCGCATCTG | TTATACGACG | AGCGCTTCGG | TCTTAACTGA | AGCAGTTAAG | 600 |
| CAATCAGATC | TTCCTTCAGG | TTATGACCAT | CTGTGCCAGT | TCGTAATGTC | 650 |
| TGGTCAACTT | TCCGACTCTG | AGAAACTTCT | GGAATCGCTA | GAGAATTTCT | 700 |
| GGAATGGGAT | TCAGGAGTGG | ACAGAACGAC | ACGGATATAT | AGTGGATGTG | 750 |
| TCAAAACGCA | TACCATTTTG | AACGATGACC | TCTAATAATT | GTTAATCATG | 800 |
| TTGGTTACGT | ATTTATTAAC | TTCTCCTAGT | ATTAGTAATT | ATCATGGCTG | 850 |
| TCATGGCGCA | TTAACGGAAT | AAAGGGTGTG | CTTAAATCGG | GCCATTTTGC | 900 |
| GTAATAAGAA | AAAGGATTAA | TTATGAGCGA | ATTGAATTAA | TAATAAGGTA | 950 |
| ATAGATTTAC | ATTAGAAAAT | GAAAGGGGAT | TTTATGCGTG | AGAATGTTAC | 1000 |
| AGTCTATCCC | GGCATTGCCA | GTCGGGGATA | TTAAAAAGAG | TATAGGTTTT | 1050 |
| TATTGCGATA | AACTAGGTTT | CACTTTGGTT | CACCATGAAG | ATGGATTTCG | 1100 |
| AGTTCTAATG | TGTAATGAGG | TTCGGATTCA | TCTATGGGAG | GCAAGTGATG | 1150 |
| AAGGCTGGCG | CTCTCGTAGT | AATGATTAC | CGGTTTGTAC | AGGTGCGGAG | 1200 |
| TCGTTTATTG | CTGGTACTGC | TAGTTGCCGC | ATTGAAGTAG | AGGGAATTGA | 1250 |
| TGAATTATAT | CAACATATTA | AGCCTTTGGG | CATTTTGCAC | CCCAATACAT | 1300 |
| CATTAAAAGA | TCAGTGGTGG | GATGAACGAG | ACTTTGCAGT | AATTGATCCC | 1350 |
| GACAACAATT | TGATT | | | | 1365 |

2) INFORMATION FOR SEQ ID NO: 230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: HUC19
 (C) ACCESSION NUMBER: Extracted from AF181950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGGGGGTTT | CTTTTAATAT | TATGTGTCCT | AATAGTAGCA | TTTATTCAGA | 50 |
| TGAAAAATCA | AGGGTTTTAG | TGGACAAGAC | AAAGAGTGGA | AAAGTGAGAC | 100 |
| CATGGAGAGA | AAAGAAAATC | GCTAATGTTG | ATTACTTTGA | ACTTCTGCAT | 150 |
| ATTCTTGAAT | TTAAAAAGGC | TGAAAGAGTA | AAAGATTGTG | CTGAAATATT | 200 |
| AGAGTATAAA | CAAATCGTG | AAACAGGCGA | AAGAAAGTTG | TATCGAGTGT | 250 |
| GGTTTTGTAA | ATCCAGGCTT | TGTCCAATGT | GCAACTGGAG | GAGAGCAATG | 300 |
| AAACATGGCA | TTCAGTCACA | AAAGGTTGTT | GCTGAAGTTA | TTAAACAAAA | 350 |
| GCCAACAGTT | CGTTGGTTGT | TTCTCACATT | AACAGTTAAA | AATGTTTATG | 400 |
| ATGGCGAAGA | ATTAAATAAG | AGTTTGTCTG | ATATGGCTCA | AGGATTTCGC | 450 |
| CGAATGACGC | AATATAAAAA | AATTAATAAA | AATCTTGTTG | GTTTTATGCG | 500 |
| TGCAACGGAA | GTGACAATAA | ATAATAAAGA | TAATTCTTAT | AATCAGCACA | 550 |
| TGCATGTATT | GGTATGTGTG | GAACCAACTT | ATTTTAAGAA | TACAGAAAAC | 600 |
| TACGTGAATC | AAAAACAATG | GATTCAATTT | TGGAAAAAGG | CAATGAAATT | 650 |
| AGACTATGAT | CCAAATGTAA | AAGTTCAAAT | GATTGACCG | AAAAATAAAT | 700 |
| ATAAATCGGA | TATACAATCG | GCAATTGACG | AAACTGCAAA | ATATCCTGTA | 750 |
| AAGGATACGG | ATTTTATGAC | CGATGATGAA | GAAAAGAATT | TGTAACGTTT | 800 |
| GTCTGATTTG | GAGGAAGGTT | TACACCGTAA | A | | 831 |

2) INFORMATION FOR SEQ ID NO: 231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4193 bases
 (B) TYPE: Nucleic acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
 (B) STRAIN: N315
 (C) ACCESSION NUMBER: Extracted from AP003129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231

| | | | | | |
|------------|------------|------------|------------|------------|-----|
| ATGAGCCGCT | TGATACGCAT | GAGTGTATTA | GCAAGTGGTA | GTACAGGTAA | 50 |
| CGCCACTTTT | GTAGAAAATG | AAAAAGGTAG | TCTATTAGTT | GATGTTGGTT | 100 |
| TGACTGGCAA | GAAAATGGAA | GAATTGTTTA | GTCAAATTGA | CCGTAATATT | 150 |
| CAAGATTTAA | ATGGTATTTT | AGTAACCCAT | GAACATATTG | ATCATATTAA | 200 |
| AGGATTAGGT | GTTTTGGCGC | GTAAATATCA | ATTGCCAATT | TATGCGAATG | 250 |
| AAAAGACTTG | GCAGGCAATT | GAAAAGAAAG | ATAGTCGCAT | CCCTATGGAT | 300 |
| CAGAAATTCA | TTTTTAATCC | TTATGAAACA | AAATCTATTG | CAGGTTTCGA | 350 |
| TGTTGAATCG | TTTAACGTGT | CACATGATGC | AATAGATCCG | CAATTTTATA | 400 |
| TTTTCCATAA | TAACATAAAG | AAGTTTACGA | TTTTAACGGA | TACGGGTTAC | 450 |
| GTGTCTGATC | GTATGAAAGG | TATGATACGT | GGCAGCGATG | CGTTTATTTT | 500 |
| TGAGAGTAAT | CATGACGTCG | ATATGTTGAG | AATGTGTCGT | TATCCATGGA | 550 |
| AGACGAAACA | ACGTATTTTA | GGCGATATGG | GTCATGTATC | TAATGAGGAT | 600 |
| GCGGGTCATG | CGATGACAGA | TGTGATTACA | GGTAACACGA | AACGTATTTA | 650 |

| | | | | | |
|-------------|------------|-------------|------------|------------|------|
| CCTATCGCAT | TTATCACAAG | ACAATAACAT | GAAAGATTTG | GCGCGTATGA | 700 |
| GTGTTGGCCA | AGTATTGAAC | GAACACGATA | TTGATACGGA | AAAAGAAGTA | 750 |
| TTGCTATGTG | ATACGGATAA | AGCTATTCCA | ACGCCAATAT | ATACAATATA | 800 |
| AATGAGAGTC | ACCCTATAAA | GTTCCGGCACT | GCTGTGAGAC | GACTTTATCG | 850 |
| GGTGCTTTTT | TATGTTATTG | GTGGGAAATG | GCTGTTGTTG | GAATTAAGGT | 900 |
| TCTATTTGAA | ATGTAAAAAA | TAATTCGATA | TTAAATGTAA | TTTATAAATA | 950 |
| ATTTACATAA | AATCAATCAT | TTTAATATAA | GGATTATGAT | AATATATTGG | 1000 |
| TGTATGACAG | TTAATGGAGG | GAACGAAATG | AAAGCTTTAT | TACTTAAAAC | 1050 |
| AAGTGTATGG | CTCGTTTTGC | TTTTTAGTGT | GATGGGATTA | TGGCAAGTCT | 1100 |
| CGAACGCGGC | TGAGCAGTAT | ACACCAATCA | AAGCACATGT | AGTAACAACG | 1150 |
| ATAGACAAAG | CAACAACAGA | TAAGCAACAA | GTAACGCCAA | CAAAGGAAGC | 1200 |
| GGCTCATCAA | TTTGGTGAAG | AAGCGGCAAC | CAACGTATCA | GCATCAGCAC | 1250 |
| AGGGAACAGC | TGATGAAATA | AACAATAAAG | TAACATCCAA | CGCATTTTCT | 1300 |
| AACAAACCAT | CTACAGCAGT | TTCAACAAAA | GTAAACGAAA | CGCACGATGT | 1350 |
| AGATACACAA | CAAGCCTCAA | CACAAAAACC | AACTCAATCA | GCAACATTCA | 1400 |
| CATTATCAAA | TGCTAAAACA | GCATCACTTT | CACCACGAAT | GTTTGCTGCC | 1450 |
| AATGTACCAC | AAACAACAAC | ACATAAAATA | TTACATACAA | ATGATATCCA | 1500 |
| TGGCCGACTA | GCCGAAGAAA | AAGGGCGTGT | CATCGGTATG | GCTAAATTAA | 1550 |
| AAACAATAAA | AGAACAAGAA | AAGCCTGATT | TAATGTTAGA | CGCAGGAGAC | 1600 |
| GCCTTCCAAG | GTTTACCACT | TTCAAACCAG | TCTAAAGGTG | AAGAAATGGC | 1650 |
| TAAAGCAATG | AATGCAGTAG | GTTATGATGC | TATGGCAGTG | GGTAACCATG | 1700 |
| AATTTGACTT | TGGATACGAT | CAGTTGAAAA | AGTTAGAGGG | TATGTTAGAC | 1750 |
| TTCCCGATGC | TAAGTACTAA | CGTTTACAAA | GATGGGAAAC | GCGCGTTTAA | 1800 |
| GCCTTCAACA | ATTGTAACGA | AAAATGGTAT | TCGTTATGGA | ATTATTGGCG | 1850 |
| TAACGACACC | AGAAACAAAG | ACGAAAACAA | GACCTGAGGG | CATTAAAGGT | 1900 |
| GTTGAATTTA | GAGATCCATT | ACAAAGTGTG | ACAGCAGAAA | TGATGCGTAT | 1950 |
| TTATAAAGAC | GTAGATACAT | TTGTTGTTAT | ATCACATTTA | GGGATTGATC | 2000 |
| CTTCAACACA | AGAAACATGG | CGTGGTGATT | ACTTAGTGAA | ACAATTAAGT | 2050 |
| CAAAATCCAC | AATTGAAGAA | ACGTATTACA | GTCATTGATG | GTCATTCACA | 2100 |
| TACCGTACTT | CAAAATGGTC | AAATTTATAA | CAATGATGCA | TTAGCACAAA | 2150 |
| CAGGTACAGC | ACTTGCGAAT | ATCGGTAAAG | TTACATTTAA | TTACCGCAAT | 2200 |
| GGAGAGGTAT | CAAATATTAA | ACCGTCATTG | ATTAATGTTA | AAGACGTTGA | 2250 |
| AAATGTAACA | CCGAACAAAG | CATTAGCTGA | ACAAATTAAT | CAAGCTGATC | 2300 |
| AAACATTTAG | AGCACAAACA | GCAGAGGTTA | TTATTCCAAA | TAATACCATT | 2350 |
| GATTTCAAAG | GAGAAAGAGA | TGACGTTAGA | ACGCGTGAAA | CAAATTTAGG | 2400 |
| AAACGCGATT | GCAGATGCTA | TGGAAGCGTA | TGGCGTTAAG | AATTTCTCTA | 2450 |
| AAAAGACTGA | CTTTGCCGTG | ACAAATGGTG | GAGGTATTCG | TGCCTCTATC | 2500 |
| GCAAAAGGTA | AGGTGACACG | CTATGATTTA | ATCTCAGTAT | TACCATTTGG | 2550 |
| AAATACGATT | GCGCAAATTG | ATGTAAAAGG | TTCAGACGTC | TGGACAGCTT | 2600 |
| TCGAACATAG | TTTAGGTGCA | CCAACAACAC | AAAAAGACGG | TAAGACAGTA | 2650 |
| TTAACAGCGA | ATGGCGGTTT | ACTACATATC | TCTGATTCAA | TTCGTGTTTA | 2700 |
| CTATGATATG | AATAAACCGT | CTGGCAAACG | AATTAACGCT | ATTCAAATTT | 2750 |
| TAAATAAAGA | GACAGGTAAG | TTTGAAAATA | TTGATTTAAA | ACGTGTATAT | 2800 |
| CATGTAACGA | TGAATGACTT | CACAGCATCA | GGTGGCGACG | GATATAGTAT | 2850 |
| GTTCCGGTGGC | CCTAGAGAAG | AAGGTATTTT | ATTAGATCAA | GTACTAGCAA | 2900 |
| GTTATTTAAA | AACAGCTAAC | ATAGCTAAGT | ATGATACGAC | AGAACCACAA | 2950 |
| CGTATGTTAT | TAGGTAAACC | AGCAGTAAGT | GAACAACCAG | CTAAAGGACA | 3000 |
| ACAAGGTAGC | AAAGGTAGTG | AGTCTGGTAA | AGATGTACAA | CCAATTGGTG | 3050 |
| ACGACAAAGC | GATGAATCCA | GCGAAACAAC | CAGCGACAGG | TAAAGTTGTA | 3100 |
| TTGTTACCAA | CGCATAGAGG | AACTGTTAGT | AGCGGTACAG | AAGGTTCTGG | 3150 |
| TCGCACATTA | GAAGGAGCTA | CTGTATCAAG | CAAGAGTGGG | AACCAATTGG | 3200 |
| TTAGAATGTC | AGTGCCTAAA | GGTAGCGCGC | ATGAGAAACA | GTTACCAAAA | 3250 |
| ACTGGAAC TA | ATCAAAGCTC | AAGCCCAGCA | GCGATGTTTG | TATTAGTAGC | 3300 |
| AGGTATAGGT | TTAATCGCGA | CTGTACGACG | TAGAAAAGCT | AGTTAAAATA | 3350 |
| TATTGAAAAC | AATACTACTG | TATTTCTTAA | ATAAGAGGTA | CGGTAGTGTT | 3400 |
| TTTTTATGGA | AAAAAGCTAT | AAACGTTGAT | AAACATGGGA | TATAAAAACG | 3450 |
| GGGATAAGTA | ATAAGACATC | AAGGTGTTTA | TCCACAGAAA | TGGGGATAGT | 3500 |
| TATCCAGAAT | TGTGTACAAT | TTAAAGAGAA | ATACCCACAA | TGCCCACAGA | 3550 |

| | | | | | |
|------------|------------|------------|------------|------------|------|
| GTTATCCACA | AATACACAAG | TTATACACTA | AAAATTGGGC | ATAAATGTCA | 3600 |
| GGAAAATATC | AAAAACTGCA | AAAAATATTG | GTATAATAAG | AGGGAACAGT | 3650 |
| GTGAACAAGT | TAATAACTTG | TGGATAACTG | GAAAGTTGAT | AACAATTTGG | 3700 |
| AGGACCAAAC | GACATGAAAA | TCACCATTTT | AGCTGTAGGG | AAACTAAAAG | 3750 |
| AGAAATATTG | GAAGCAAGCC | ATAGCAGAAT | ATGAAAAACG | TTTAGGCCCA | 3800 |
| TACACCAAGA | TAGACATCAT | AGAAGTTCCA | GACGAAAAAG | CACCAGAAAA | 3850 |
| TATGAGCGAC | AAAGAAATTG | AGCAAGTAAA | AGAAAAAGAA | GGCCAACGAA | 3900 |
| TACTAGCCAA | AATTAAACCA | CAATCCACAG | TCATTACATT | AGAAATACAA | 3950 |
| GGAAAGATGC | TATCTTCCGA | AGGATTGGCC | CAAGAATTGA | ACCAACGCAT | 4000 |
| GACCCAAGGG | CAAAGCGACT | TTGTATTTCG | CATTGGCGGA | TCAAACGGCC | 4050 |
| TGCACAAGGA | CGTCTTACAA | CGCAGTAACT | ACGCACTATC | ATTCAGCAAA | 4100 |
| ATGACATTCC | CACATCAAAT | GATGCGGGTT | GTGTTAATTG | AGCAAGTGTA | 4150 |
| TAGAGCATTT | AAGATTATGC | GTGGAGAAGC | ATATCATAAA | TGA | 4193 |

2) INFORMATION FOR SEQ ID NO: 232

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2996 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Staphylococcus aureus
- (B) STRAIN: 85/2082
- (C) ACCESSION NUMBER: Extracted from AB037671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232

| | | | | | |
|-------------|------------|-------------|------------|------------|------|
| ATGAAACGAG | CCATTGGTTA | TTTGCGCCAA | AGTACAACGA | AACAACAATC | 50 |
| ACTCCCAGCT | CAAAAGCAAG | CAATAGAATT | ATTAGCTCCA | AAGCACAATA | 100 |
| TTCAAAATAT | CCAATACATT | AGTGATAAGC | AATCAGGCAG | AACAGATAAT | 150 |
| CGAACAGGCT | ATCAACAAGT | CACCGAACGC | ATCCAACAAA | GACAATGTGA | 200 |
| CGTATTATGT | TGTTATCGCT | TGAATCGACT | TCATCGCAAC | TTGAAAAATG | 250 |
| CATTAAAACT | CATGAAACTC | TGTCAAAAAT | ATCATGTTCA | TATTCTAAGT | 300 |
| GTTTCATGAT | GCTATTTTGA | TATGGATAAA | GCGTTTGATC | GCCTAAAAC | 350 |
| CAATATATTC | ATGAGTCTGG | CTGAACCTGA | ATCCGATAAT | ATTGGAGAAC | 400 |
| AAGTCAAAAA | TGGACTTAGA | GAAAAGGCAA | AACAAGGTAA | ACTCATAACG | 450 |
| ACCCATGCGC | CTTTCGGTTA | TCAC'TATCAA | AATGGTACTT | TCATCATTTA | 500 |
| TAATGATGAA | TCACCTACCG | TCAAAGCTGT | ATTCAATTAT | TATCTTCAAG | 550 |
| GATATGGCTA | CAAGAAGATT | GCACAATATT | TAGAAGACGA | TAATAAACTT | 600 |
| ATTACCCGCA | AGCCTTATCA | GGTACGAAAT | ATAATTATGA | ACCCAAATTA | 650 |
| TTGTGGTCGT | GTCATCAATC | AATATGGTCA | ATATAACAAT | ATGGTACCAC | 700 |
| CTATTGTTTC | GGCAACGAAA | TATGAACATG | CTCAAGCAAT | CCGTAATAAG | 750 |
| AAGCAACTTC | ACTGTATACC | TTCAGAGAAT | CAGCTGAAAC | AAAAGATCAA | 800 |
| ATGTCCTTGT | TGTGACTCAA | CACTGACAAA | TATGACAATA | AGAAAAAAAC | 850 |
| ATACATTGCG | ATATTATATT | TGTCCTAAAA | ATATGAATGA | ATCTCGCTTT | 900 |
| GTCTGTTTCAT | TCAAAGGAAT | AAATGCACAA | AAATTAGAAG | TTCAAGTCTT | 950 |
| AGCTACATGT | CAGAACTTCT | TTCAAAACCA | ACAGCTCTAT | TCAAAAATTA | 1000 |
| ATAATGCAAT | TCATCAACGC | CTCAAAAAAC | AAAGAGTGAT | AGAAGCTAAA | 1050 |
| AGTACGCTAA | CTCAAGAACA | ACTGATAGAT | AAACTTGCCA | AAGGTATGAT | 1100 |

| | | | | | |
|-------------|-------------|------------|------------|-------------|------|
| TGATGCTGAA | TCATTCAGAA | AACAGACTCA | TTTGATGAAT | CAAAAGCACA | 1150 |
| AAACCATATC | CTCCATAAGT | GATAATCAGT | TACAAACATC | ACTACAAAAG | 1200 |
| GTTATACAGA | AAAGTTTCAC | GTTAAACATG | CTGCATCCCT | ATATTGATGA | 1250 |
| AATTCGCATT | ACAAAAAATA | AAGCCCTTGT | TGGGATCTAT | TTCAAAAATG | 1300 |
| AACCATTGAA | CATTGTGAAC | CAAACCTCGC | AATCATCGAT | TGCTTAATCA | 1350 |
| GAAAGGATGA | AAAAATCATG | CAACAACTCA | AACAAAAACG | TGTCGGTATC | 1400 |
| TATGTTTCGTG | TATCAACGGA | AATCCAAAGT | ACTGAAGGCT | ATAGTATCGA | 1450 |
| TGGACAAATC | AATCAAATTC | GAGAATATTG | TGATTTCAAT | AACTTTGTTG | 1500 |
| TTGTAGATGT | ATACGCGGAT | AGAGGTATCT | CTGGAAAATC | TATGAACCGA | 1550 |
| CCAGAACTAC | AACGTTTGT | AAAAGATGCG | AACGAAGGTC | AGATTGATTC | 1600 |
| TGTTATGGTC | TACAAAACAA | ACCGACTAGC | ACGTAACACT | TCTGACTTAC | 1650 |
| TCAAAATTGT | TGAAGACCTT | CATCGTCAAA | ATGTCGAATT | CTTCAGCTTA | 1700 |
| TCTGAGCGTA | TGGAAGTCAA | TACAAGCAGT | GGTAAATTGA | TGCTACAAAT | 1750 |
| TCTAGCGAGT | TTTTTCAGAAT | TTGAAAGAAA | TAATATTGTC | GAAAATGTAT | 1800 |
| TCATGGGTCA | AACCCGACGC | GCTCAAGAAG | GCTATTATCA | AGGCAATTTG | 1850 |
| CCGCTGGGCT | ATGACAAAAT | ACCGGATAGC | AAGCATGAAC | TCATGATAAA | 1900 |
| CCAACATGAA | GCGAATATTG | TCAAATATAT | ATTTGAGTCA | TATGCTAAAG | 1950 |
| GCCACGGATA | TCGTAAAATT | GCGAATGCAC | TCAATCACAA | AGGATACGTG | 2000 |
| ACTAAAAAAG | GAAAGCCTTT | CAGTATTGGT | TCAGTGACCT | ATATCTTATC | 2050 |
| TAATCCATTC | TATGTTGGTA | AAATTCAATT | CGCAAAGTAC | AAAGATTGGA | 2100 |
| ATGAAAAGCG | TCGTAAAGGG | CTGAATGATA | AACCAATAAT | AGCTGAAGGT | 2150 |
| AAGCATTCCC | CTATTATTAT | TCAAGACTTA | TGGGATAAAG | TCCAATTACG | 2200 |
| TAAAAAACAA | GTCAGTCAAA | AACCTCAAGT | CCACGGTAAA | GGAACATAATC | 2250 |
| TATTAACAGG | TATCGTTCAT | TGTCCACAAT | GTGGTGCACC | AATGGCAGCT | 2300 |
| AGTAACACAA | CGAACACATT | GAAAGATGGT | ACCAAGAAGC | GAATACGTTA | 2350 |
| TTATTCTTGC | AGTAACTTCC | GAAACAAAGG | CTCAAAAGTA | TGTTCTGCGA | 2400 |
| ATAGCGTTAG | AGCTGATGTG | ATTGAGAAAT | ACGTCATGGA | TCAAATACTC | 2450 |
| GAAATTGTCA | AAAGTGATAA | AGTCATTAAC | CAAGTCTTAG | AACGTGTCAA | 2500 |
| TCAAGAAAAT | AAAGTCGATA | TTGGTGCATT | GAACCACGAT | ATCGCTTATA | 2550 |
| AACAACAACA | ATACGATGAA | GTCAGCGGGA | AACTCCATAA | TTTAGTTAAA | 2600 |
| ACCATTGAAG | ATAATCCGGA | CCTAACATCT | GCATTGAAAG | CAACTATTCA | 2650 |
| TCAATATGAA | ACACAACCTCA | ATGACATTAC | AAATCAAATG | AATCAACTCA | 2700 |
| AACAGCAACA | AAATCAAGAG | AAACTATCTT | ATGATACGAA | ACAAATCGCT | 2750 |
| GCCCTATTAC | AACGAATATT | TCAAAATATA | GAATCAATGG | ATAAAGCACA | 2800 |
| ACTCAAAGCA | TTATATCTTA | CAGTCATTGA | CCGTATTGAT | ATTCGTAAAG | 2850 |
| ACGGTAATCA | TAAAAAACAG | TTCTACGTTA | CACTAAAAC | CAATAATGAA | 2900 |
| ATTATTAAAC | AACTTTTCAA | TAATACCCCT | CTCGACGAAG | TGCTCCTCAG | 2950 |
| CACTTCGTCT | TTATTTTTCG | CTCAAACGCT | CTTTCTTCAA | ATCTAA | 2996 |

2) INFORMATION FOR SEQ ID NO: 233

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1410 bases
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: Genomic DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*
- (B) STRAIN: CCRI-9681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233

| | | | | | |
|-------------|------------|-------------|------------|------------|------|
| GCTGTAGGGA | AACTAAAAGA | GAAATATTGG | AAGCAAGCCA | TAGCAGAATA | 50 |
| TGAAAAACGT | TTAGGCCCAT | ACACCAAGAT | AGACATCATA | GAAGTTCCAG | 100 |
| ACGAAAAAGC | ACCAGAAAAT | ATGAGCGACA | AAGAAATTGA | GCAAGTAAAA | 150 |
| GAAAAAGAAG | GCCAACGAAT | ACTAGCCAAA | ATTAAACCAC | AATCCACAGT | 200 |
| CATTACATTA | GAAATACAAG | GAAAGATGCT | ATCTTCCGAA | GGATTGGCCC | 250 |
| AAGAATTGAA | CCAACGCATG | ACCCAAGGGC | AAAGCGACTT | TGTATTGTC | 300 |
| ATTGGCGGAT | CAAACGGCCT | GCACAAGGAC | GTCTTACAAC | GCAGTAACTA | 350 |
| CGCACTATCA | TTCAGCAAAA | TGACATTCCC | ACATCAAATG | ATGCGGGTTG | 400 |
| TGTTAATTGA | GCAAGTGTAT | AGAGCATTTA | AGATTATGCG | TGGAGAAGCA | 450 |
| TATCATAAAT | GATGCGGTTT | TTTCAGCCGC | TTCATAAAGG | GATTTTGAAT | 500 |
| GTATCAGAAC | ATATGAGGTT | TATGTGAATT | GCTGTTATGT | TTTTAAGAAG | 550 |
| CATATCATAA | GTGATGCGGT | TTTTATTAAAT | TAGTTGCTAA | AAAATGAAGT | 600 |
| ATGCAATATT | AATTATTATT | AAATTTTGAT | ATATTTAAAG | AAAGATTAAG | 650 |
| TTTAGGGTGA | ATGAATGGCT | TATCAAAGTG | AATATGCATT | AGAAAATGAA | 700 |
| GTACTTCAAC | AACTTGAGGA | ATTGAACTAT | GAAAGAGTAA | ATATACATAA | 750 |
| TATTAAATTA | GAAATTAATG | AATATCTCAA | AGAAGTAGGA | GTGTTGAAAA | 800 |
| ATGAATAAGC | AGACAAATAC | TCCAGAACTA | AGATTTCCAG | AGTTTGATGA | 850 |
| GGAATGGAAA | AAAAGGAAAT | TAGGTGAAGT | AGTAAATTAT | AAAAATGGTG | 900 |
| GTTCAATTGA | AAGTTTAGTG | AAAAACCATG | GTGTATATAA | ACTCATAACT | 950 |
| CTTAAATCTG | TTAATACAGA | AGGAAAGTTG | TGTAATTCTG | GAAAATATAT | 1000 |
| CGATGATAAA | TGTGTTGAAA | CATTGTGTAA | TGATACTTTA | GTAATGATAC | 1050 |
| TGAGCGAGCA | AGCACCAGGA | CTAGTTGGAA | TGACTGCAAT | TATACCTAAT | 1100 |
| AATAATGAGT | ATGTACTAAA | TCAACGAGTA | GCAGCACTAG | TGCCTAAACA | 1150 |
| ATTTATAGAT | AGTCAATTTT | TATCTAAGTT | AATTAATAGA | AACCAGAAAT | 1200 |
| ATTTCAAGTGT | GAGATCTGCT | GGAACAAAAG | TGAAAAATAT | TTCTAAAGGA | 1250 |
| CATGTAGAAA | ACTTTAATTT | TTTATCTCCT | AATTACACTG | AACAACAAAA | 1300 |
| AATAGGTAAT | TTCTTCAGCA | AACTCGACCG | CCAGATTGAG | TTAGAAGAAG | 1350 |
| AGAAACTTGA | ACTCTTATAG | CAACAAAAGC | GTGGATATAT | TTCAGAAGAT | 1400 |
| TTTTCTCAAG | | | | | 1410 |

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/CA 02/00824

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, MEDLINE, EMBL, EMBASE, PAJ, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
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| Y | ITO T ET AL: "Structural comparison of three types of staphylococcal cassette chromosome mec integrated in the chromosome in methicillin-resistant Staphylococcus aureus." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES MAY 2001, 'Online! vol. 45, no. 5, May 2001 (2001-05), pages 1323-1336, XP002238384 ISSN: 0066-4804 cited in the application page 1334, left-hand column, paragraph 3 -right-hand column, paragraph 2; figures 1,2; tables 1,2 page 1335, left-hand column, paragraph 2 page 1335, right-hand column, paragraph 2 | 1-20 |
| X | -& DATABASE EMBL 'Online! 14 May 2001 (2001-05-14) retrieved from EBI -/-- | 14, 17, 18 |



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
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- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *B* document member of the same patent family

Date of the actual completion of the international search

15 April 2003

Date of mailing of the international search report

24.09.03

Name and mailing address of the ISA

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Authorized officer

Rutz, B

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| | Database accession no. AB037671 XP002238391 abstract --- | |
| X | DATABASE EMBL 'Online! 7 January 2000 (2000-01-07) retrieved from EBI Database accession no. AB014433 XP002238392 abstract --- | 14,17,18 |
| Y | EP 0 887 424 A (KAINOS LAB INC) 30 December 1998 (1998-12-30) page 3, line 2 - line 10 page 4, line 28 - line 35 page 6, line 30 - line 34; figures 1-3,5,8 --- | 1-20 |
| A | HIRAMATSU K ET AL: "Genetic Basis fo Molecular Epidemiology of MRSA" J INFECT CHEMOTHER, vol. 2, 1996, pages 117-129, XP001122060 cited in the application page 120, left-hand column, paragraph 2 -right-hand column, paragraph 1; figures 2,4 page 122, left-hand column, paragraph 1 page 123, right-hand column, paragraph 1 -page 124, left-hand column, paragraph 1 --- | |
| A | OLIVEIRA D C ET AL: "Genetic organization of the downstream region of the mecA element in methicillin-resistant Staphylococcus aureus isolates carrying different polymorphisms of this region." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUL 2000, vol. 44, no. 7, July 2000 (2000-07), pages 1906-1910, XP002238385 ISSN: 0066-4804 page 1906, left-hand column, paragraphs 1,2; figures 1,2; tables 2,3 page 1908, right-hand column, paragraphs 1,2 page 1909, left-hand column, paragraph 3 -right-hand column, paragraph 3 --- | |
| A | ITO T ET AL: "Cloning and nucleotide sequence determination of the entire mec DNA of pre-methicillin-resistant Staphylococcus aureus N315." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUN 1999, vol. 43, no. 6, June 1999 (1999-06), pages 1449-1458, XP002238386 ISSN: 0066-4804 --- | |

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| A | KATAYAMA Y ET AL: "A new class of genetic element, staphylococcus cassette chromosome mec, encodes methicillin resistance in Staphylococcus aureus." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY. UNITED STATES JUN 2000, vol. 44, no. 6, June 2000 (2000-06), pages 1549-1555, XP002238387 ISSN: 0066-4804 --- | |
| A | KURODA M ET AL: "Whole genome sequencing of methicillin-resistant Staphylococcus aureus" LANCET THE, LANCET LIMITED. LONDON, GB, vol. 357, no. 9264, 21 April 2001 (2001-04-21), pages 1225-1240, XP004246103 ISSN: 0140-6736 page 1234, right-hand column, paragraph 3 page 1238, left-hand column, paragraph 3; figure 1 --- | |
| P,X | MA XIAO XUE ET AL: "Novel type of staphylococcal cassette chromosome mec identified in community-acquired methicillin-resistant Staphylococcus aureus strains." ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, vol. 46, no. 4, April 2002 (2002-04), pages 1147-1152, XP002238388 April, 2002 ISSN: 0066-4804 cited in the application figures 1,2 & DATABASE EMBL 'Online! 21 November 2001 (2001-11-21) retrieved from EBI Database accession no. AB063172 abstract & DATABASE EMBL 'Online! 21 November 2001 (2001-11-21) retrieved from EBI Database accession no. AB063173 abstract --- -/-- | 1-20 |

INTERNATIONAL SEARCH REPORT

International Application No

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| P,X | <p>OLIVEIRA D C ET AL: "The evolution of pandemic clones of methicillin-resistant <i>Staphylococcus aureus</i>: identification of two ancestral genetic backgrounds and the associated mec elements."</p> <p>MICROBIAL DRUG RESISTANCE (LARCHMONT, N.Y.) UNITED STATES 2001 WINTER, vol. 7, no. 4, January 2001 (2001-01), pages 349-361, XP009004903 ISSN: 1076-6294</p> <p>cited in the application page 352, left-hand column, paragraph 4 -right-hand column, paragraph 5; figure 1; tables 2,3 page 355, left-hand column, paragraph 6 -right-hand column, paragraph 4 & DATABASE EMBL 'Online! 8 March 2002 (2002-03-08) retrieved from EBI Database accession no. AF411934 abstract & DATABASE GENBANK 'Online! 5 March 2002 (2002-03-05) retrieved from NCBI Database accession no. AF411935 abstract & DATABASE GENBANK 'Online! 5 March 2002 (2002-03-05) retrieved from NCBI Database accession no. AF411936 abstract</p> <p style="text-align: center;">---</p> | 1-20 |
| P,X | <p>BABA TADASHI ET AL: "Genome and virulence determinants of high virulence community-acquired MRSA."</p> <p>LANCET. ENGLAND 25 MAY 2002, vol. 359, no. 9320, 25 May 2002 (2002-05-25), pages 1819-1827, XP002238389 ISSN: 0140-6736</p> <p>page 1823, left-hand column, paragraph 2 -right-hand column, paragraph 1; figures 2-4; tables 1,2 & DATABASE EMBL 'Online! 27 May 2002 (2002-05-27) retrieved from EBI Database accession no. AP004822 abstract</p> <p style="text-align: center;">---</p> <p style="text-align: center;">-/--</p> | 1-20 |

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/CA 02/00824

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| P, A | <p>HIRAMATSU KEIICHI ET AL: "The emergence and evolution of methicillin-resistant <i>Staphylococcus aureus</i>." TRENDS IN MICROBIOLOGY, vol. 9, no. 10, October 2001 (2001-10), pages 486-493, XP002238390 page 492, right-hand column, paragraph 2; figures 1-5; table 1 -----</p> | |

INTERNATIONAL SEARCH REPORT

International application No.
PCT/CA 02/00824

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/SA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type iv, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type iv, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type iv

Invention 2: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type v, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type v, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type v

Invention 3: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type vi, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type vi, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type vi

Invention 4: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type vii, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type vii, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type vii

Invention 5: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type viii, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type viii, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type viii

Invention 6: claims 1-20 (all partially)

nucleic acids derived from Staphylococcus aureus MREJ type ix, oligonucleotides hybridizing with said nucleic acids, oligonucleotide pairs for the detection of MREJ type ix, method to detect the presence of methicillin-resistant Staphylococcus aureus of MREJ type ix

FURTHER INFORMATION CONTINUED FROM PCT/SA/ 210

Invention 7: claim 1 (partially)

method to detect the presence of methicillin-resistant
Staphylococcus aureus of MREJ type x

Invention 8: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type i

Invention 9: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type ii

Invention 10: claim 15 (partially)

oligonucleotide pairs for the detection of MREJ type iii

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/CA 02/00824

| Patent document cited in search report | Publication date | Patent family member(s) | Publication date |
|-------------------------------------------|---------------------|----------------------------|--------------------------|
| EP 0887424 | A | 30-12-1998 | JP 9224700 A 02-09-1997 |
| | | | AU 696462 B2 10-09-1998 |
| | | | AU 1810997 A 10-09-1997 |
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| | | | EP 0887424 A2 30-12-1998 |
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